

# **FIGURE 1**

ACTGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCACCGCGTCCGGGCGGAGCACGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCTGCGCCGGAGGCCAAAGAAGCCGACGCCCTGCCACCGGTGCCGGGCT  
CTGCTGCCGCCGCGCCGGAGGCCAAAGAAGCCGACGCCCTGCCACCGGTGCCGGGCT  
GGTGGACAAGTTAACCAGGGATGGTGACACCGCAAAGAAGAAGAACTTGGCGGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTAGCAGTCAGCAGATTGCCGTGGAGATC  
CTGGAGGGCTGTGCGAGAGCAGCAGCTTCAATGCAATCAGATGCTAGAGGGCAGGAGGA  
GCACCTGGAGGGCTGGTGGCTGAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC  
CAGGGCGGATCCCAGGGCCCTGCAGCGGGATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGCGCAGGGTCTGCCGGTGCACATGGGTACCAAGGGCCGCTGTGACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCTGACCAACAGAGACTGCGGGAGTGTGAAGTGGCTGGTGCT  
GGACGAGGGCGCTGTGTTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCTACAGTGGAAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAGAGTGTATCTCTGGCTACGCAGGGAGCA  
CGGACAGTGTGCAAGATGTGAGCAGTGCCTACTAGCAGAAAAAACTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGCTGTGTTCTGACGGCTTCGAAGAACG  
GAAGATGCCCTGTGCGCCGCCAGGGCTGAAGGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCCTTAAATTATTCAAGAGATGTCC  
CGTGGAAAATGTGCCCTGAGGATGCCGTCCCTGCAGTGGACAGCGGGGGAGAGGCTGC  
CTGCTCTCAACGGTTGATTCTCATTGCTCTTAAACAGCTGCATTCTGGTTGTCTTA  
AACAGACTTGATATTTGATACAGTTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGGCCGCACTTGTGTTATTGAGCTTATAATGGTTACAATAAGCAATAGCA  
TCACAAATTCAAAATAAGCATTGTTCACTGCATTCTAGTTGTGGTTGTCAAACCTC  
ATCAATGTTATCTTATCATGTCGGATCGGAATTAATTCCGGCGCAGCACCATGCCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTCTGAGGGCGAAAGAACCGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCAGCAGGCAGAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPERRAALGLPLLLLPPAPEAKKPTPCCHRCRGLVDFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLYVCCSPGTYGPDCLAQGGSQRPCSG  
NGHCSDGDSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCSGLTNRDCGECEVGWLDE  
GACVDVDECAAEPFFCSAAQFCKNANGSYTCCECDSCVGCCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPAAEAEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

### **FIGURE 3**

CAGGTCCAAC TG CAC CCT CGG TCT AT CG ATT GA AT T C C C G G G A T C C T T A G A G A T C C T C  
GAC CT CG ACC C A C G C G T C C G C A C C G G A G G C G A C C G C C C A G C C G T C T A A C C G G A A C A  
G C C T G G C T G A G G G A G C T G C A G C G C A C G A G G A T T C T G A C G C C C G G A C C G T C G A G G T G C G  
G C A C G A G G A G G A T T T C C G G C A G G C A G G A G G T C T G A C G A C G A T E G C C C G G A G G A G C C T T C  
C C T G C C G C C G C T C T G G A G C A T C C T C T G T G C C T G T G G C A C T G C G G G C G G A G G C  
C G G G C C G C C G C A G G A G G A G G C C G T G A C C T T A T G G A T C G A T G C T C A C C A G G C A A G A G T A C T C A  
T A G G A T T G A G A G A G A T T A T C C T G A T T G T T C G A G G G G A A A T T G G C A C C T T T A C A C G A T G A T  
T T C A G A A A A G C G C A C A G A G A T T G C C A G G T A T T C C T G T C A A T T C A T T C C A T G A A T T T C A  
C T G G C C A G C T G C A G G G C A G G C A G A A T A C T T C A T G A A T T C C T G T C T T G C G C T C C C T G G A T A  
A A G G C A T C A T G G C A G A T C C A A C G T C A A T G C T C C T C T G T C G G G A C A C T G G C C T C A C A A G G C A  
T C A G G T T G C A A G G T G T T C C C A T G T C T G G G G A A A A C C G A T G G G G T G C G A C T T A G G A A G T  
G G A T G T G A T T G T T A G A A T T C T G A A G G C A C A C C A T T C T C C A A C A C C T C A A A T G C T A T C T  
T C T T T A A A A C A T G T C A A C A C G T C A G G T G C C C A G G C G G G T G C C G A A A T T G G G A C C T T T G T A A T  
G G A A G C A G C T C T G C G A G G T G T C T G T C G A T G G G T T C C A C C G A C T C A T G T G A G A A G G C C T T T G  
T A C C C C A G A T G T A G A T G G T G A C T T T G T G A C T T C T G G T A T T C T G C A T C T G C C C A C T G  
G A T T C T A T G G A G T G A A C T G T G A C A A A G C A A C T G T C A A C C A C T G C T T T A T G G A G G G A C C  
T G T T T C A T C C T G G G A A A A T G T A T T G G C C C T C C A G G A C T A G G G G G A G G A C T G T G A A A T C A G  
C C A A T G C C C C A C A C C C T G T G C A A T G G G A G G T T A A A G C A A T G T G A A T G T G T  
C C A A A G G T T A C C A G G G A G A C C T C T G T C A A A G G C T G T C G C G A G G C T C G C T G T G G T C C A C A T  
G G A A C C T G C C A T G A A C C C A A C A A T G C C A A T G T C A A G A G G T T G G C A T G G A A G A C A T G C C A A  
T A A A A G G T T C A G A G G C C G C T C A T A C G T C C T G A G G G C C A G C C G G C C C G A C T C A G G C A C  
A C A C G C C T T C A C T T T A A A A G G C C G G A G G C C G C G G G A T C C A T G A A T C C A A T T A C A T C T G  
T G A A C T C C G A C A T C T G A A C G T T T A A G T T A C C A A G T T C A T A G C C T T G T T A A C C T T C A  
T G T G T G A A G T T G C C A A A T A T G T C T T A T T C A C T T A C T T A A G G A A T A T C G G C C T G A A T T T T A T T A G C T  
T C A T T A A A A T A T C A T C G A G G T G T G A T A T T T A C T T C C T T T A A G G T T T C A T A G T A C G T C T G T A G  
C A T G A T G G T A T A G A T T T T C T G G T T C A G G T G C T T G G G C A G A G T T T A T T A T T A T T G T C A T A T G G T  
T C A G G T T T A A A A T T T C A G T G T G A T G G T G C A G A T A T T T C A A A A T T A C A T G C A T T T A T G G T  
G T C T G G G G G C A G G G G A A C T C A G A A A G G T T A A A T T G G C C A A A A T T G G C T G A A T G C C A A G A A T  
T T G G A T G T G C G A T G T T A A T G T G A A G G T T A C A G C C T T G C A G A T T T T A T T G T C A G A T T A T T G A G A T  
G T T T G T T A C A T T T T A A A A A T T G C T C T T A A T T T T A A A C T C T C A A T C A A T A T A T T T G A C C  
T T C A T T A A T T C C A G A G A T T C A G T T A A A A A A A A T T A C A T C T G T G T G A T G T G C C A T T  
A A A C A T T A A T A T A T A T C T C A A C A A T G A A A T T G G G A A T T A G T G A A C T T T T G C A T  
T G G C T G A A G C A A T T A A T A T A T T G T A A C C A A A C A C G C T C T F A C T C A A T A A C A T T T T A T  
A C T G T T T G T A T G T A T A A A A T A A A G G T G C T G C T T T A G T T T T T G G A A A A A A A A A A A A A A A A A  
A  
C G G C A T G C C C C A A C T T G T T T A A T G C A G C T T A A T A A C A T T A A T A A T A A T A A T A A T A A T A A T A A T G

## **FIGURE 4**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094  
><subunit 1 of 1, 379 aa, 0 stop  
><MW: 41528, pI: 7.97, NX(S/T): 2  
MARRSAFPAAALWLWSILLCLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNINHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
RNNGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPKVC  
EPGCGAHGTCHEPNKCQCQBGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGCGTCGGCGGTGCGAGAGCCAGGGAGGGGGAGGCAGCGCGGGGAGCCTGGG  
CCCCAGCCCACACCTTCACCAAGGGCCAGGAGCCACCATGTGGCATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCCTGGGACTTGCTCTGGGTCGCCAGCAGGGTCTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGATCCGGGACGGCGGGAGGGCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGTGCCAGCAGCTGCTGCCACTGGGCGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCACTTGACTCTGGGACTTC  
TGCCCTGGCGTGCCACCCCTTTCCCCGATCCAAGGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGAAACGTACTGGGAAACTGTAAACCGTTGACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCAGACATCAAAGGCCATCAACCGGGCAACTATGGCTGCCAGGCTGG  
GAACACAGGCCCTCTGGGCATGACCTGGAGGGATTGCTACCAGGCCCTGGGACCA  
TCGGCCATCTCTCGGTATGAAACATGATGAAATTATAACTGCTGAACCCAGGGAG  
GTGCTTCCCACAGCTTCGAGGCCCTTGAGAAAGTGGCCAACCTGATTATGAGGCCCTTG  
CCAAGGCAACTGTGCAAGGCTCTGGGCCCTTCCACAGCACGCTGTCGATCGATCTGCT  
CAATCCATTCTGGGACAATGACGCCCTCTGTCGCCCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGGCTCGAGCAGCTGATGGCTGGGCTCTGGCTCG  
CCGAGGGGGTGGTCTGACCATCTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGC  
CTGCGCCCCCTGTATGATGACAGCGAGGCATGGGCTGGGCAAGGCCAGGCCACTGCC  
CACTGCCCCAACAGCTATGTTATAAACATGACATCTACAGGCACTCTGTCTACCGCCT  
CGGCTAACGACAAGGGAGATCATGAGGGACTGTAGGAGAATGGCCCTGTCCAAGCCCTA  
TGGAGGTGCACTGAGGACTTCTCTATACAAGGGAGGACATCTACAGGCCACGCCAGTGA  
CTTGGAGGGCCAGAGGAGATACCGGCCGATGGGACCCACTCAGTCAGATCACAGGATGGG  
AGAGGGAGGGCTGCCAGATGAGGGACGCTAAATACTGGACTGCCGCAACTCTGGGCC  
CAGGCCCTGGGGAGAGGGCAACTTCCGATCTGCGCCGGCTCAATGAGTGCAGACATGAG  
AGCTTCTGCTGGCGCTCTGGGCCGCTGGGAGATGGAGACATGGGCTCATCACTGAGGCTG  
CGGGCACCCGGGGTCCGGCTCAGGCTAAGGGCCGGGAAGAGGGCCCAATG  
GGGGCGTGTGACCCCGACCTCGCCGACAGGCCCGGGGCCAGGGGGGCCAGGGCGTAAT  
CCCGGCCGGGTTCCGCTGACGCAAGGCCCGCTGGGAGGCCGGGCCAGGGCGAGACTGGC  
GAGCCCCCAGACCTCCAGTGGGACGGGCAGGGCTGGCTGGGAAGAGCACAGCTCAG  
ATCCCAAGGGCTCTGGGCCCTGGGAGACAGCACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCGATTCTTTTTTTAGACAGGGCTCTGGCTCG  
TTGCCCAAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCACTCTGGGTC  
AGTACCCCTCCACCTCAGCCTCAAGTAGCTGGGACTACAGGTGCAACCCACACTTGGC  
TAATTTTGATTTTGAAAGAGGGGCTCACTGTGCTGCCAGGCTGGTTCAGACT  
CCTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGGATTGCAAGGCTAGGCC  
ACTGACCCAGCCCTGATTCTTCAAGTATTCTTCAAGTATTCTTCACTGTTTAAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCTTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCCTGTCCTTNGCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGCAGNTGGCGTCTCGATGGTGCCCTGGTGGTTCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGCCCTGCGC  
CCCCCTGTATGATGACAGCCGACATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTCTCCTATACAAGGGAGGCATCACAGCCACACGCCAGTGAGCCTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## FIGURE 8

GCTGCTTGCCTGTGATGGCAGGCTTGGCCCTGCAGCCAGGACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCCTGACCCTGACAGCAAAGGCTG  
CAGCTGAAC TGCGTGGATQACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT  
GGCCTGCTCCCTGCACTCGGCTGCTGCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCAGTGGA GGCCTGTCCTGGTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGGCCCTCTCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTTAACCCGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCGACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACCTGGA  
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCTGGAGGCTGGAGGAA  
GGGGCCAGGCCACATTCTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA

## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDT  
DPPADGPSNPLCCCFHGPFAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCACCGCGTCCGAACCTCTCAGCGATGGAGCCGCCCTGCTGCCAACCTCACTCTGT  
GCTTA CAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC  
GACCAGCTGAGCAGGGCGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTCAGGTACCGGGCGTCGCATCTCCGCCACCGGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGCACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGGAAAGCCCAGCGGGAAAGAGCAAAGACTG  
CGTGGTCACGGAGATCGTGTGGAGAACAACTATA CGGCCCTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGCCCTCACGGGCAGGGGGGCCCGCCAGGCTTCCCGCAGGCCAGAAC  
CAGCGCAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCAACCACGC  
CGAGAACGAGAACAGCTCGAGTTGTGGCTCGCCCCCACCGCCGGACCAAGCGCACAC  
GGCGGCCAGCCCCACGTAGTCAGGGAGGCAAGGGGGCAGCAGCCCCCTGGCCGCTCC  
CACCCCTTCCCTCTTAATCAAGGACTGGGCTGGGTGGCGGGAGGGAGCCAGATCCCC  
GAGGGAGGACCTGAGGGCCCGAAGCATTGAGCCCCCAGCTGGAAAGGGGAGGCCGGTG  
CCCCAGGGCGCTGGCACAGTGCCCTTCCGGACGGGTGGCAGGCCCTGGAGAGGA  
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC  
CGCTGAAAGGTCAAGCAGTGAAGGCCCTTGAGACAAACCGCTGGAGGTGGCTGTCCCTAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTAGCCCCAACCTCTCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAAAGAAAGGGAGAGAGGAAATAG  
AGGGTTGTCACCTCACATTCCACGACCCAGGCCCTGCACCCCAACCTCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLIGKPSGKSKDGVFTIEIVLE  
NNYTAFQNARHEGWFMADFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCACATGGAG  
GACAGCAGCAAGAGGGCAACACAGGCTGATAAGACCAGAGCAGCAGGGAGATTATTCTAC  
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTTCTGGACTTCACAGAACCCATCCAGT  
CATTTGATTTCTGTTTATTTTTTCTTTCTTCTTCCACACATTGTATTTTAT  
TCCCCTACTTCAGAAATGGCCTTACAGACCAAAGTGGCCAGCCATGGCTTCTTCT  
GAAGTCTTGGCTTATCATTCCTGGGGCTACTCAGGCTCCAACTCCTGGCTGCC  
CTAGTGTGTGCCGTGCGAAGGAACCTTGCTACTGTATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCCGGAGGGCTAACCGTACTACCTCCACAACAACCAAATTAAATAATGCG  
TGGATTCTCTGAGAACCTGACAATGTAACAGCTGGTACACCGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAGAAATGTCAAGGTTCTCCATTGAGAAAAC  
AAATTAGGACCATTCAGGCTGCTCTGGCCAGCTCTTGAAAGGAGCTGACACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGCAGGGCCCTCCGGGAGGCTATTAGCC  
TCAAAATTGTTGTTTGTCTAAGAATCCTGAGCTGCTGCTATCCGACATGGCTTCCAGAA  
TTGCAAGAGCTGAGAGTGGATGAAAATCTGAAATTGCTGTCTATCCGACATGGCTTCCAGAA  
TCTCACGAGCTGGAGCTTATTGTGGACGGGAAACCTCTGACCCAACAAGGGTATGGCG  
AGGGCACCTCAGGACATCTCACCAAGCTAACGAAATTTCATGTACCTAATTGCTGTCC  
CACCCCTCCCTCCGATCTCCAGGTACGCATCTGATCAGGCTTATTGAGGACAACAGAT  
AAACACCATCCCTTGACAGCCTTCTCAAATCTGCTAAAGCTGGCTGAAAGCTGGATATACCA  
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ATATATCCCTCATCTCAACGTGCGGGTTTGTGACCAAGGTCTGAACAAGTCCGG  
GGATGGCCGTGAGGAAATTAAATGAAATTGGCTCTGTCCTCCACACGGACCCCGCTG  
CCTCTCTTCACCCCAGCCCCAGTACAGCTCTGGACCAACTCAGCCTCCACCCCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCCTAACCTACCCACATCGAAACTTCCACGATT  
CTGACTGGGATGGCAGGAAAGACTGGCCACCTATTCTGTAACGGATCCAGCTCTATC  
CATTGGTGAATGATACCTCAAGTCAAGCTGGCTCTCTCTTCCACCGTGATGGCATA  
CAAACTCACATGGGTGAAATGGCCACAGTTAGTAGGGGGCATGTTAGGAGGCATAG  
TCACGGTAGAGAACACAACCTGAGGCTGGTAACCTAGAGCCCCGATCCACCTATCGATT  
TGTAGTGGCCTGGGATGCTTTAACTACCGCGCGGTAGAGAACACCATTTGTTAGAGGC  
CACCAACCCATGCCCTCATCTGAAACACGGCAGAACACAGCGTCCAGGGATGAGCAGCGA  
CGTCCCACAGCATGGGCTCCCTTCTGCTGGCGGCTTGATCGGGGGCGGGTATATT  
GTGCTGGTGGCTTGCTCAGCGCTTTGCTGGCATATGCAACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAAACGGGGCCGGGAAAGATGATTATTGCGAGGCAGGCACAAAGA  
AGGACAACCTCCATCTGGAGATGACAGAAACCGATTTCAAGATGTCCTTAAATAACGAT  
CAACTCTTAAAGGAGATTTCAGACTGCAAGCCATTACACCCAAATGGGGCATTAATT  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTCCAGACCTGGAGC  
ACTGCCATACCTGAGCAGAGGCCAGCGTTATCAAGGCGACAAATTAGACTCTTGGAGAA  
CACACTCGTGTGACATAAAAGACACGCAGATTACATTGATAATGGGATTTAAAAAGTG  
CTATCTTCTATTCAAGTTAACAAACAGTTGTAACCTTGTCTTTAAATCTT

# **FIGURE 13**

MGLQTTKWPSPHGAFFLKSWLIIISLGLYSQVSCKLLACPSVRCDRNFVYCNERSLTSVPLGIP  
EGCIVTFLYLNHNQINNAGFPAAELHNQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDDENSISTVGVEDGAFREAIISLKLFLSKNHLSSPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQRLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARELNMNLLSCPTTTPLFLFTP  
APSTASPTQPPTLSIPNPSSRSYTPPTPTTSKLPTIPDWDRGRERVTPPISERIQLSIHFVND  
TSIQVSWLSSLFTVMAYKLTWVKMGSLSVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVP  
DAFNRYRAVEDTICSEATHASYNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQWKYNRGRKDDYCEAGTKKDNSILEMTETSQIVSLSNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

## FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGHRHARTHQPQTALESSCENKRADLVFIDSSRSVNTHDYAKVEFIVDILQFLDIGPDVTTRVGLLQYGSTVKNEFSLKTFKKRSEVERAVKMRHLSTGTMGLAIQYALNIAFSEAE GARPLREN PVRVIMIVTDGRPQDSVAEVAAKARDTGILIFAI GVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHFCINIPGSYVCRCKQGYI LNSDQTTCRIQDL CAMEDHNC EQLCVNVPGSFVCQCYSGYA LAEDGKRCVAVD YCASENHGCEHBCVNADGSYLCQC HEGFALNPDEKTC TRINYCALNKPGCEHECVNMEE SYYCRCHRGYTLD PGNKTC S RVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI NEDLKTCSRVDYCLLSDHGCEYS CVNMDRSFACQCPEGHVLRS DGK TAKLDSCALGDHGCE HSCVSSEDSFVCQC FEGYI LREDGKTC RRDV CQAIDHGEHICVNNSDSYTCECLEGFRLA EDGKRCRRKDVKC STHHGCEHICVNNGNSYICKCSEG FVLAEDGRRCKCTEGP IDLVFVID GS KSLGEENFEVVKQFVTG I DLSLTISPKAARVGLLQYSTQVHTEFTL RNFNSAKDMKKAVA HMKYMKGKGSMTGLALKHM FERSPTQEGE GARPLSTRVPRAIAVFTDGRAQDDVS E WASKAKAN GITMYAVGVGKAIEEELQEIA SEPTNKHLYAEDFSTMDEI SEKLKGKICEALEDSDGRQDS PAGE LPKTVQ QPTESEPVTINI QDLLSCSNFAVQHRYLFEDDNLLRSTQKL SHSTKPGSPL EEKHDQCKCENLIMFQNL ANEE VRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGGGCTGGCTCCCGCGCACGCTCCGGCCGCGCAGGCCG  
GCACCTGCAGGTCCGTGCGTCCCAGCGCTGGCGCCCTGACTCCGTCGGTTTGTTCTGGGCTGA  
**CATGATTCCCTCCGGGCCCCCTGGT**GACCAACTTGCTGCGGTTTGTTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCACCGGTTGCGAG  
GCGGTGGAGGGAGGGAAAGTGGTCTTCAGCGTGGTACACCTTGACCGGGAGGTGCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAAGGAGGATC  
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCACTCC  
ATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGTCTCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAGGAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTAAGTGGTCTCCAGCTCTCATCTGCCGTCTCCAGGGTGTGCCCAT  
GTGGGGCAACAGTGAACCTGAGCTGCCAGTCTCAAAGGAGTAAGCCCGCTGCAATACCA  
GTGGGATCGGAGCTCCATCTCCAGACTTCTTGACCCAGCATTAGATGTCATCGTG  
GGTCTTAAAGCCTCACCAACCTTCTGCTTCCATGGCTGGAGTCTATGTCGAAAGGCCAC  
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTTGACCTGGTGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGATACCACCCCCGGGGCAAGGCCCTGGAGGAGCCAGCAATGATACTAAGGAGGATGCC  
ATTGCTCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAAATGGGACCC  
TTCCTCTGTCACCTCCGACCGAGCCCTGCCACCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGGCCAGGGCTGCCCTACCAAGACTGCCACGACAGAT  
GGGGCCACCCCAACCAATCCCCATCCCTGGTGGGTTCTCCCTCTGGCTTGAGCCG  
CATGGGTGCTGTCCTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGTTCTCTCCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCGTGAGTCATGGGAAAGAGTCACACTCCGTACCCCTAGTACTCTGCCCTCACCTC  
TTTACTGTGGAAAACCACATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAAGGAGAAGAGGA  
AGTGGATCTGAAATTGGGAGGAGCCCTCCACCCACCCCTGACTCCCTTATGAAGCCAGTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTCTCCAGGC  
CCCCCTGATCTGACCCACCCCTATCTAACACCCACCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTGGTAGGTTACTGGGCAGAGGATAGGGATCTC  
TTATTAACATGAAATATGTGTTTTCTTGCAAATTAAATAAGATACTAA  
TGGTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLOEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRQLQGVPHVGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSSLTNLSSMAGVYVCKAHNEVGTAQCNVTLLEVSTGPGAA  
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEPANDIKEADAIAPRTLWPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISPIPGVSSSGLSR  
MGAVPVMPVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 18

GGCCACCACTGCGGCCACGCCAATGAAACGCCCTCCGCCCTAGTGGTTTTCCACCTTG  
TTGAATTGTCCTATACTCAAATTGCAACAGACACCTGTCTCCAAATGCAAATGTGA  
AATACGCAATGGAATTGAAAGCCTGCTATTGCAACATGGATTTCAGGAAATGTGTCACAA  
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCTGTGGGAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTGTATGTGACCTGGCTTCAAGATCCAGCAGTAACCA  
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACCTGCCATT  
TAGATAATGTCGTATAGCTGCAAAATTAAATAAAACTTAAACAAAATCAGATCCACAAAAA  
GAACCTGTGGCTTCTACAAGAAGCTATAAGAAAATCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAATATTAGCTGAATCATCTCATTACTAGTTACAAGAACACA  
CTATCTCAGCCAAGGACACCCCTCTAACTCAACTCTTACTGAATTGAAAAACCGTGAAT  
AATTGTGTCAAAGGGATACTTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACATGCAACACTGTGAAACAAGCTTTAAGGATATCCCAGGCTTCC  
AAAAGACCCACAGAGTTGTACAAATTCAACGGATAATGCTCAAAGTTCTTTTGAT  
TCATATAACATGAAACATATTCTCATATGAATATGGATGGAGACTACATAAAATATATT  
TCCAAAGAGAAAAGCTGATATGCAATGCAATGCACTTGCAAGTGGCATTTTTATATA  
AGAGTATTGGCTCTTGTCTTCATCTGCAACACTTCTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTCAGTAATTCTCAGTCTCAATGACCTCAAACCC  
ACCACCAATTATGAACTTGAAGAAAATAACATTACATTAAAGTCATCGAAAGGTCACAGATA  
GGTATAGGAGTCTATGTGCAATTGGAATTACTCACCTGATACCATGAAATGGCAGCTGGTCT  
TCAGGGCTGTGAGCTGACACTAACTGAGACCCACACCTCATGCCGCTGTAATCACC  
GACACATTGCAATTGATGTCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTC  
TTACAAGGATCACTCAACTGAAGAATTAAATTCTACTGATTGTTGCTTGCATATT  
ACCTTCTGGCTCTTCAGTAATTCAAGGCCAGGACAACATTCAACAAATCTTGTG  
TAGCCTATTCTGTGCTGAATTGTTTCTGTGTTGGATCAATCAAATACTAATAAGCT  
TCGTGTCATATTGCCGAGCTCTACACTACTCTTTTAGCTGCTTTGCATGGATGTGC  
ATTGAAGGCATACATCTCATCTATTGTGTTGGTGTCTACAAACAAAGGGATTGGCA  
CAAAGATTTTATCTTGGCTATCTAACGGCCAGCGTGTGAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCAACACAAAGTATGTTGGCTTAGCACCAGAAAACAATT  
TGGAGTTTATAGGACAGCAGCATGCTTAATTCTGTGTTATCTCTGGCTTTGGAGTCAT  
CATATACAAAGTTCTGCTCACACTGCAAGGGTTGAAACCAAGATTAGTTGCTTGGAGACA  
TAAGGCTTGTCGAAGAGGCCCTCGCTCTGTGTTCTCTGGCACCACCTGGATCTT  
GGGGTTCTCCATGTTGCAACGCCACTAGGTGTTACAGCTTACACTCTCAGTCAGCAATGC  
TTCCAGGGATGTTCATTTTATTCTCTGTGTTTATCTAGAAAAGTTCAAGAAGAAT  
ATTACAGATTGTCAAAATGCCCCCTGTGTTGGATGTTAAGGTAAACATAGAGAAATG  
GTGGATAATTCAACACTGCAACAAAATAAAATTCCAAGCTGTGGATGACCAATGTAAAAAA  
TGACTCATCAAATTCCAATTATTAACACTAGACAAAAAGTATTAAATCAGTTTCT  
GTTTATGCTATAGGAACCTGAGATAAAAGTAAATTGATCATATAGATAACTATGT  
TTTTCTATGTGAAATAGTTCTGCAAAATAGTATTGAGATATTGGAAAGTAATTGTT  
CTCAGGAGTATCACTGCCACCAAGGAAGATTCTTCTAACACAGAGAAGTATGAA  
TGTCTGAAGGAAACACTGGCTTGTATTTCTGTGACTCGTGTGCTTGGAAAACACTAGTCC  
CCTACCCACCTCGGAATGAGCTCATTACAGAAAGCTGCAACATAAGAGAATGAAGGGCAGA  
ATATCAAAACAGTGAAGAGGAATGATAAGAGATGTATTGAAATGAACTGTGTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACAAAAAAAGAATTGAGAAACACATTACCTTACATTGAA  
TTGTTCTGAACTTAAATGTCACCTAAACACTTAGACTCTGTGCTTAATCTGTTCTT  
TTTCTAATATTCTAAAAAAAAAAAGTTTACCTCCACAAATTGAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVТИCEDDNEC  
GNLTQSCGENANCTNTEGSYCMCVPGRFSSSNQDRFITNDGTVCIENVNANCHLDNVСIAA  
NINKTLTKIRSIKEPVALLQEVRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL  
NSTLTLTETFKVTVNNFVQRDTVVWDKLSVMHRRTHLTKLMHTVEQATLRISQSFKTTEDFT  
NSTDIALKVFFFDSYNMKHIHFMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPKQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELTYSNETHTSCRCHLTHFAILMSSGPGSIGIKDYNILTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAEVFLVGINTNTNKLFCSSIAGL  
LHYFFLAAFAFMNCIEGHLYLIVVGVIYNKGLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT  
TKVCWLSTENNFIFIWSFIGPACLIILVNLLAFGVIIYKVFRTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVHASSVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCAGTCATGAGCTCAAACCCACCCAC  
ATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCATGTGGCATTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATTTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC  
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

## FIGURE 21

GTCTCCAGCCAAGAACCTCGGGGCCGTCGGCGGGTGGGGAGGAGTCCCCCGAAACCCGGCG  
CTAAGCGAGGCCTCCTCCTCCCGAGATCCGAACGGCTGGCGGGCTCACCCCGCTGGGA  
CAAGAAGCCGCGCCTGCCTGCCGGGGCCGGGGAGGGGCTGGGCTGGGGCTGGGGCGAGGCGG  
GGTGTGAGTGGTGTGCGGGGGGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TCTCTGGCCACCTACCCGTGGGGCCGTAAGGGCTACTATATAAGGCTGCGGGCCGGAG  
CCGCCGCGCGTCAGAGCAGGGCTCGCTCCAGGATCTAGGGCCACGACCATCCAAACCC  
GGCACTCACAGCCCCCAGCGCATCCGGTCGCCGCCAGCCTCCGACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCA**ATGCGGAGGGGTGTGTGGTCCACGTATGG**  
ATCCCTGGCGGGCCTGGCTGGCGGCCGGCCCTCGCCCTCGGACGCCGG  
CCACGTGCACTACGGCTGGGGCACCACCGCTCGCCGACCTGTACACCTCGGGGG  
ACGGGCTCTCAGCTGCTTCTCGCGCATCGTGCACGGCTGTGACTGCCGCCGGGC  
CAGAGCGCGCACAGTTGCTGGAGATCAGGCACTGCGCTGCGGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGGCTACCTCTGCATGGCCCGAGCGGAAGATGCAAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGTTTCAGGGAGGAGATCCGCCAGATGGCTACAATGTGACCGA  
TCCGAGAACGCCGACCCGCTCCCGTCTCCGAGCTGGCAAAACAGGGCAGCTGTAACAGAA  
CAGAGGCTTCTTCCACTCTCATTTCTGCATGCCCCATGTCAGGAGACGGCTG  
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTTCGCCCTGGAGACGGACAGCATG  
GACCCATTGGGCTTGTCAACCGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAG**TAAGT**  
GAGACCATGCCGGGCTCTTCACTGCTGGCAGGGCTGGTACCTGCAAGGGCTGGGAGC  
TGCTCTACAAGAACAGTCTGAGTCCACGGTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTGTGATATTTAGAGTTTCAATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT  
CATAAACATTGTAAGCTGTAGCTTGGCCACGCTGCTGGGGCCCCATTCTGCTCCCTCGA  
GGTGTGCTGGACAGCTGCTGCACTGTCAGTTCTGCTGAAATACCTCCATCGATGGGAAC  
TCACTTCTTGGAAAATTCTTATGTCAGCTGAAATTCTCTAAATTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCACTGTTAATTCAAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAATTTCACTCAACCCCATGTCAGGGATTGATCTATATCTACTTCAGGG  
ACCATTTGCCCTTCCCAAATCCAGGCCAGAACTGACTGGAGCAGGATGGCCACAGG  
GCTTCAGGAGTAGGGGAAGCTGGAGGCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC  
CTGAGGGCAGTTCTGTCATGGATGCTGTCCTGGAGAATAACTTGTGCTGTCGGGTGTCACCTGC  
TTCCATCTCCAGGCCACGCCCTGCCCCACCTCATGCTCCCTGGGATTTGATGGGCT  
CCCAGGCCCCACCTTATGTCACCTGCACTTCTGTCAGGAAATTGATCTATATCTACTTCAGGG  
TTGAAGACCCCAAGTCTGTCAATAACTTGTGTCAGGGAAAGACCTAGAAC  
CTTTCCCCCAGCAGTGGTTTCAACATGATATTATGACTAATTATTTGATATGTACA  
TCTCTTATTTCTTACATTATTATGCCCCAAATTATATTATGATGTAAGTGAGGTTG  
TTTTGTATATTAAGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLPLSVLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCGAGAAGTTCAAGGGCCCCGGCTCCTGCGCTCCTGCGCGCCGGACCTCGACCTCTCA  
GAGCAGCCGGCTGCCGCCGGAAAGATGCGAGGAGGAGCCGCCACCGCCTCCTCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGTATCATAAGGCATATGGTTTCTGCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCTGCAAACCCAA  
AGAACAGACTGTTCCCTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGCTCTTGTCTAC  
TATCAACAGACTCTTCAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGGCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCAGTCAGTGGAAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAGA  
CAAAGAAGGGAAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCCAGACTTGGCTCCAAACGACCAACAGCTCATACAAATGAATACAAAAGTGGAACT  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATTCTGTGAAGGCCGCAATT  
TGGTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCGTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGCTACTTTCAAAAGAAACCTCTCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCACTGGCTCACGCCGTAAATCCCAGCACTTGGAGG  
CCGGCGGGCGGATCAGGAGTCAGGAGTTCTAGACCAGTCTGGCAATATGGTGAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGCATGGGGCATGTGCGCTGCAGTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATA  
ATAAAATACTGGTTTACCTGAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLRLVVALGYHKAYGFSAPKDKQQVVTAVEYQEAIACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TWTLEVVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGINLLLENPRLGSQST  
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAAGAG  
AAAAGAAGAGGAAGATGTTGGCAACATTATAACATGCTCCACGCCGGACCTGGCAT  
CATGCTGCTATTCTCTGCAAATACTGAAGAACATGGGATTAAATATTACTCTAAATAA  
ATGAATTACTCAATCTCTATGACCCTATACATACTCCACCTCAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTACCTTCTCTTCAATCAGCTCTATTGAACCTACTGACTG  
CAATTGTGCACTGCACTTATTCTAGTGAAAGAAAATTGCTATGGCATTCTATCA  
TTTGACAATGCAAGCATCTCTTCTATCAATCAGCTCTATTGAACCTACTGACTG  
TGAATTCCTTAAGGGCCCATTTCTGAAAGAAAGCTAAAGATGAAGGACATGCCACT  
CGGAACTCATGTGCTACTTGCCCTAGCTATCACTACAGTACAAGCTGTAGATAAAAAG  
TGGATTGTCCACGGTTATGACGTGTGAATCAGGCCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAAATGATTAGGTCTTTAACTTTCCAGGCCAGATTGCC  
AGCTAACACACAGATTCTCTCTCACAGCTAACAAATATGCAAAATTTGAATACTCCACAG  
ACCTTCCAGTAAACCTTACTGGCTCTGGATTATTCTCAAAACAAATTATCTTCACTGACCAAT  
ATTAATGAAAAAGATGCCCTAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA  
ACTGCCCTTAAAGGAAATGCTGTCGAACTGCAACTTACAGAAACTCTATTTAAATCACAACT  
TGCCTTCTCACATTTCACCTGGAGCCCTTATTGGCTCATATAATCTTCTTGACTTCATCTC  
AATTCAAATAGATTGCAAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAAACTTAGAGAT  
TCTGATGATTGGGGAAATCCTAAATTAGAATCAAAGACATGAACTTTAAGCCTTATCA  
ATCTTCGAGCCTGGTTATAGCTGGTACAGGAACTTACAGGAAACAGATAACGCCCTGGTT  
GGACTGAAAACCTTAGAGAACGATCTCTTTACGATAACAGGCTTAAAGTACCCCAGT  
TGCTCTTCAAAAAGTTGTAATCTCAAATTGGATCTAAATAAAAATCTTAAATAGAA  
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTTGGGATAAAAATATGCT  
GAGGCTGATTTCACATGAGTCTGCTGCTGGATAACCTGGCAGATTAAAGAAAATAGAAC  
TACTAACACCTAGATTGCTTACATTCAACCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAAACAGCAATGCTCTGACTGCTGGCTTGACCTGGTACCTGGTCTG  
CCAAACCTCAAGGAAATCAGCATAACAGTAAACCCCATCAGGTGTGACTGTGCTCCTGG  
GATGAACATGAACAAAACACATTGATTCTGGAGCCGATTCACTGTTTGCCTGGACC  
CACCTGAATTCAAGGTCAAGATGTTGGCAAGTGCAATTTCAGGGACATGATGAAATTGT  
CTCCCTTCTTATAGCTCTGGAGCTTCTCTAATCTAAATGAGTAAAGCTGGGAGCTATGT  
TTCCCTTCTTCACTGTAGAGCTACTGCGAGAACCCAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAACCTTCTGCTTAACCTCTGACAGACAAGTTCTATGTCATTCTGAGGGAAACACTA  
GATATAAATGGGCTAACTCCAAAAGAAGGGGTTTATATACTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAACTGTGTTATGATCAAAGTGGATGGATCTTCCACAGATAACATG  
GCTCTTGAATTTAAAGAGATACTCAGGCCATTCACTGTTTGGTGTCTGGAAAGCA  
AGTTCTAAAATCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCCTGCGAAAGTGCCTGCAATACCATCTGATGTCAAGGTATATAATCTACTCATCTGAAATC  
CATCAACTTGAGTATAAAATTGTTATGATATTCCACCATCTATCAGAAAACAGAAA  
TGTGTAATGTCACCAACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGCCCTGCTGGAGGCTCTGGGGATTATTGGTGTGATATGCTTATCA  
GCTGCCCTCTCCAGAAAATGAACTGTGATGGGGACAGCTATGTGAGGAATTACTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAATCTCTGGGAAGCAGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTATAGGTTACCAACAAATATGCTC  
AAAAACCCACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MDKMPPLRIHVLLGLAITTLVQAVDKVKDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLLQTNNIAKIEYSTDFPVNLTGQLDSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELNSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQLQMINSKWFD  
LPNLEIILMIGENPIRIKDMNFKPLINLRLSLSVIAGINLITEIPDNALVGLENLESISFYDRL  
IKVPHVALQKVVLNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNNPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSDLFCVDPPFQGQNVRQVHFRDMMEICLPLIAFPSPSNLV  
EAGSYVSFHCRTAEQPQEYIWITPSGQKLLPNTLTDKFYVHSECTLINGVTPKEGGLYTC  
IATNLVGAIDLKVSMIKVDGSPFQDNNGSLNPKIRDIQANSVLVSKASSKILKSSVKWTAFV  
KTEENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKCVNVTTKGLHPDQE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSILKVATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACCGCTTGGAGTAGATGAGGAATGGGCTCGTGAATTGTCGACATTCCAGCATGAATCT  
GGTAGACCTGTGTTAACCGCTTCCCCTCCATGTGTCCTCCTACAAAGTTGTTCTTA  
TGATAGCTGCTTCATTCTGCCAGTATGTGTCCTAACGGGCTGTTGTTCTCCTCTGGG  
GGTTAAATGTCACTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTAACCTGTCACAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGCAAGACTCTGGACTTGTCGACAATCGGATTCAAAG  
TGTGCAAAAAATGCCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCAATCATGAGACAGCCAC  
AACGTGATCTGAAACGTCGTGTTGGATGAAACATGTCGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAACTCCCTAAAAAAACTACCGATTATGCCATGCTGGCACCA  
TGTGTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGAGAAAGCAGATGA  
ACCTGATGATAATTAGCACTGTGGTATAGTTGCAAACACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTTGCAGTTGCAGTAGAAATAAGTGGTTACTCTCCCATCCATTGAAACATTGAA  
ACTTTGTATTTCACTGTTTTGAAATTATGCCACTGCTGAACCTTAAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATGAAATTATTTTTT  
AATTAAAAGCAAATAAAAGCTAACCTTGAACCATGGAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLQSFLMILCFHSASMC PKGCLCSSGGLNVTCSANLKEIPRDL  
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVNL SKNGIEFIDEHAFKGVAETLQTLDSLDR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHEAHNVICKTSVLDEHAGRPF  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## FIGURE 29

# **FIGURE 30**

MQVSKRMLAGGVRSSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDGKNRIFTLNQDEFASFPHLEELNEENIVSAVEPGAFNNLFNLRTL  
GLRSNRLLKLIPLGVFTGLSNTLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNLDLVYISHRA  
FSGLNSLSQLTLEKCNLTSIPTTEALSHLHGIVLRLRHILNINAIRDYSFKRLYRLKVEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGNLNYLRVLNVSGNQLTLEESVFHSVGNLETLLDSNPLA  
CDCRLLWVFRWRRLNFNRQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDSMPAHLHVRSYSPDWPHPQPNKTFAFISNQGEGEANSTRATVPFFDIKTLL  
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNLIEIYEYPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCCACCGCGTCCGCACCTCGGCCCCGGGCTCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC  
AGGGAGCGGCCGGGAAGCGCGATGGGGGCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC  
TCTTCGCTCTGCTGGCGCCGGCGGGCAACCTCTCCAGGACAGCCAGCCTGG  
ACATCTGATGAAACAGTGGGGCTGGTGGCACCGTGGTCAAGTGCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCACAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGGAGTACACCTGCTCAATCTTCACTATGCCGT  
GCGAAGTCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCTGGTT  
ATAAAATCTTCAATTACGGGAAAAAGACACGCCACCTAACTGTCACTTCTGGAGCAAG  
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCCACGGAGAACCAACCCGAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCACTGGTACATTCCAGGTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTCTGTGAACCATGAATCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCAATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCAGAAGCTGTACACTGTGAGGGTGCACGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGGT  
GCCCTGATCTTCCCTTCTCAACAAGAGTGAAGCTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGCAGCTACAAGGCCACTACACCCATGTAAATGACCCAGTCCGGTGCCT  
CTCCCTCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTTCTGCTG  
CTCATCATGCTCATCTCTGGCCACTACTTGATCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAGGCTCCGACGATGCTCCAGACGCCACACGGCCATCATCAATGCAAGAGCG  
GGCAGTCAGGAGGGAGCACAAGAAGGAATATTCATCTAGAGGGCCTGCCACTTCTGC  
GCCCCCCAGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCCGCTTGTCTCCCCAGCCACCCACCCCGTGTACAGAATGTC  
TTGGGTGCGGGTTTGTACTCGGTTGGATGGGAGGGAGGGAGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTTCTGCAATTGGTTATTATTATTGTAACATCC  
CAAATCAAATCTGTCAGGCTGGAGAGGCAAGGCCCTGGGTGAGAAAAGCAAAACAA  
AACAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFFACCWPGGANLSQDDSQPWTSDETVVAGGTVVLCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCAACCCCTTCTCTCCTTCTGG  
CTTCGGACATTGGACACTAAATGAACCTTGAAATTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAATGCTGTTGGATTCTGTT  
GCTGGAGACGCTCTTTGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAGATGAGATAGAAGGGGACCTACAGCTGAGCTGGTGAAGAAAAGG  
AGTCGAGCGTTCACTGCCCGACTTCCAGTTTACCATTTATCTGATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTTCGTAACCTTTATAATGCGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCTCCGGGGCTTTCTGGGCTGAGCTGGTGAAGAAGG  
CTGCACATCAACAAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCAGGCTGATTAAATTACAGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAAACAAGCTGAGGTCGCTATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTCATCACCCCTGCACCTCCGGGTAACAGGGCTGAAAACGCTG  
CTATGAGGAGCTTGGAGCAATTCCCTGTTATTGCGAGATCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAACATTCCAAGAATGCC  
CTGATGCCGAGCTGCTGGAGGCCCCAACAGCTGAGCTGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGCTTGGAAACCCAGTGGTGGATTCTAGTCTCCGGCGCCCTG  
CCAAGAAGAGACCTTGTCTTGACCCCTGCAACTCTTCAAGACAATGGCAAGAG  
GATCATGCCAACACAGGGCTGCTCCAAACCGAGGTAAAGATCCAGGCAACTGGCAGAT  
CAAATGACCCCCACAGCAGGATAGCAGGGTAGCTCAGGAAACAAACCCCTAGCTAAC  
GTTTACCCCTGCCCTGGGGCTGAGCTGCCAACATCCAGGGTGGTTAAAGATGAAAC  
TGCACAAACAGGAACGTGAGCAGCTGGCTGATTGAAAGCCCAAGCTCTAACGTGAGGA  
GCTTTCTCTAGAGATAACAGATCCACAGCATCGAAATTCGCAACTTGTGATTCAAGA  
ACCTCATTCTGTTGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACAGCTGTCCGGGA  
GAAATTCTCGGGGCTGCAAACCTAGAGTACCTGAACTGGAGTACAACGCTATCCAGCTCA  
TCTCTCCGGCACTTCAATGCCATGCCAACACTGAGGATCTCATTCAACAAACACCTG  
CTGAGGCTCTGCTGTGGACGGTGTCTGGCTGGGGCTCGCTCTCAAACCTAGCGCTGCAA  
CAATTACTTCACTGACCTCCCGTGGCAGGGTGCTGGACCAGTTAACCTCATCCAGA  
TAGACCTCCAGGAAACCCCTGGAGTGTCTCTGGCACAATTGCTGGCTTCAAGCAGTGGCA  
GAACAGCTTGGGGCTCGAAGTGTGATGAGCAGCCTCAAGTGTGAGACGCCGTGAACCTT  
TAGAAAGGATTTCATGCTCTCCAATGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACTGTAACCTGGCAGAATGGGGACTGGGGAGACGGGAGCAGCACTCC  
AACTCTTACCTAGAACACAGCAGGGTGTCACTCTCGTCTGGTCCCCGGACTGCTG  
GTTTGTACCTCCGCTTACCGTGGCATGCTGTGTTTACCTGAGGAACCGAAAGC  
GGTCCAAGAGACAGAGATGCCAACTCTCCCGTCCAGAGATTAAATCCCTACAGACAGTCTG  
GACTCTCTACTGGCACAATGGGCTTACAACGAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTACTCGCTCTGAGTAAGACCCCAACCCCAATAGGGAGGGAGGGAGGG  
ATACATCCTCCCCACCGCAGGCCACCCGGGGCTGGAGGGCGTGTACCAAATCCC  
CCATCAGGCCCTGGATGGGATAAGTAGATAAAATACCTGTGAGCTGCACAACCGAAAGGG  
GACCCCTTACTTAGCTCCCTCTGGAAACAAAGAGCAGACCTGTGGAGAGCTGGAGAGCG  
GCCAGCTGCTTGTGAGAGCCCTTGTGACAAAGCCAGCAGGCCCTGTGGAG  
AACTGACAGTGGCCCTCGCCCTGGCCCCGGGCTGTGGGGTTGATGCCCGGTTCTATAC  
ATATACATATATCCACATCTATAGAGAGATAGATATCTATTTCCTGTGGATTAG  
CCCCGTGATGGCTCTGTGGCTACGCAGGATGGCAGTTGCAAGAAGGCATGAATGT  
TGTAAATAAGTAACCTTGACTTCTGAC

# **FIGURE 34**

MLLWILLLETSCLCFAAGNVTDVCKEKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNFANFYNAVSLHMENNLHIEIVPGAFQLQLVKRLHINNNKIKSFRKQ  
TFLGLDDDBYQLQADFNLLRDIDPGAFQDNLKLEVILLNNDNLISTLPANVFQYVPITHDLRG  
NRLKTLPLYEEVLEQIPIGIAEILLEDDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLMNETTEQDLCPLKNRVDSSLPAPPAAQETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANSLCPGGCSDHIPGSGLKMNCCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHISRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQLNLEYLNVEYNAIQLILEPGTFNAMPKLRILILNNNLRLSLFVDVFAVGVL  
SKLSLHNYYFMYLFVAGVLQDQLTSIIQIDLHGNPWECSCTIVPFQKWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPLTSHSKNSTGLAETGTHNSYLDTSRVSISV  
VPGLLLVEFTSAFTVVGMLVIFLRNRKRSKRNDARSSASEINSLQTVCDSSYWHNGPYNADG  
AHRYVDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCA CGGGG CCTGG CAGCG CT CGC ACAC AT TCT GT CG CGC TA AGGGAA ACT GT TGGC  
CGCTGGGCCGCGGGGGATTCTTGGCAGTGGGGGCTCGTGGAGGGAGGGCGGAGGGCGGAGGG  
AAGGGAGGGGGAAACGGGGTTGGGAAGCCAGCTGTAGAGGGCGTGAACCGCGCTCAAGACAC  
AGCTCGCGTCTCGAGCGGGACAGATCCAAGTGGAGCACGCTCGCGTGGGGCTCAG  
AGAATGAGGCCCGCTCGCCCTGTGCCTCTCTGCAGCGCTCTGGCCGGCGCTCG  
CGGGCAACACCCACTGCGCACCGTGTGCTCGCCTCGGGGCTGCTACAGCTGC  
ACCACGCTACCATGAAGCGGCAGGCCGGAGGCGCTGCACTCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGGGGCGCAGCTCGCGCTGTGCTCGCCTCTGCAGGCCAGG  
GCCCGAGGGGCTCAAAGACTGTGTTCTGGGTGCACTGGAGCGCAGGCCAGTCCACT  
GCACCCCTGGAGAACGAGCTTCTGGGGGTTCTCTGTGCTCTCCGACCCCGGGCGTCTC  
GAAGCGACACGGCAGCTGGGGTGGAGGAGCCCAACGCTCTGCACCCGGCGAGATCGC  
GGTACTCCAGGGCACCGGTGGGGTCAAGGCCGGAGCTGGAGGAGATCGATGCCACCTGC  
GGCACAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTCTGCGCGCGCCCCGG  
GCCGCTCTAAGCTTGAGCTATGCCGCCCTTCAGCTGCACAGGCCGCTCTGGACTCTAG  
TCCACCTGGGACCCAGGGTAGGTGCGCTTGCGGGAGAGCTCCGATCTCAGTTACTTGA  
TCGCGGACGAATCGGCGCTCGTGGGACAACACTCTCGGGCATGTGTTGTGCCCC  
GGGAGGTACCTCCCTGTGCGGAAATGCGCAGAGCTCCCTAAGCTGCTAGACGACTTGGGAGG  
CTTGGCTGCGAATGCTGCTACGGGCTTCAGCTGGGGAAAGGACGGCCGCTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGAGGGGGTGCACCCAGGGCGCGGGCCACT  
GCAACCCAGCCCCGTGCCGAGAGAACATGCCAATCAGGGTGCAGAGAACGCTGGGAGAGAC  
ACCACTTGTCCCTGAAACAAGAACATCTGAGCTAACATCTTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGCTACCTTCTAAATGCTCCCTCAAGGGAGTCAAAGGCCACTATACC  
CCATCAGGGAGCGTGAATTCCAAGTTAAATTCTACGACTCTCTGCACTCTCAGGCTT  
CGACTCTCTCTGCGTGTCTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGTATCT  
TGACCATGACAGTACTGGGGCTGTCAAGCTGTGTTCAAGAAAGGCCCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCCGGGCCTGGAGAGTGTACCTTGAGCCCCCTGCTTGGCTC  
CAGTTCTGCACATTGCAAAACAATGGGTGAAAGTGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTGTGGCGAGTCCCCTTGGCTTAAGTGTGCA **TAGGAAACAGGGGA**  
CATGGGCACTCTGTGAACAGTTTCACTTTGTGAAAGGGAAACAGAGGAACCTTAC  
TTGTGTAACTGACAATTCTGAGAAATCCCCCTTCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAAACTGCAACTCTTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTGTAGGA  
TGGTGTACTGGGGACGGGTAGTGCTGGGGAGAGATTTCTTATGTTATTGAGAA  
TTGGAGAAGTGATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACAA  
TTAAAAAATAATTCTACAAAATGAAAGGAAATGTTCTATGTTGTTCAAGGCTAGGAGTAT  
ATTGGTTGCAATCCAGGGAAAAAATAAAAAATAAAGGATTGTTGAT

# **FIGURE 36**

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVIALLRLAGPGPGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCSTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG  
ASNLSSYRAPFQLHSALDFSPPGTEVSALCRGQLPISVTICADEIGARWDKLSGDVLCPCPG  
RYLAGKCAELPNCLDDLGCFACECATGFELGKDGRSCVTSGEQQPTLGGTGVPTRRPPATA  
TSPVPQRTWPPIRVDKEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVIFIVFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR  
KESMGPPGLESDEPAALGSSAHCTNNGVKGDCDLRDAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCTCAGGGAAACTAAG  
CGTCGACTCAGACGGCACCATATACTGCCCTTTAAAAGTGCCTCCGCCCTGCCGCCCGATTC  
CCCCGGCTACCTGGCGCCCGCGCGGGTGCAGCGCTGAGAGGGAGCGCGCGGGCAGCGA  
GCGCCGGTGTGAGCAGCCTGCTGCCAGTGTGAGCGGGGTGTGAGCGCGGGTGGGTGCGGA  
GGGGCGTGTGCGCGCGCGCGCGGGTGCAGCGCTAACCGGAGCTCTCGCCCAATGCA  
GGGGCGGAAACGCCCTGGGCCACTCTGCCCTGCTGCCCTGCCGCCACCCAGCTCGCCG  
CAGCAGTCCCCAGAGAGACCTGTTTCACTATGGTGGCATTCTTAATGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGGTGACCTCCAATAGCAAATGTAATTGGAAAAATCA  
CAGTTCCCGAAGGAAAAGTAGCTGTTCTAACATTCCGATTCAAGACCTCGAGAGTGAAAC  
CTGTGCCGTATGACTTGTGGATGTGTACAATGGCCATGCCAATGGCAGCGCATTGGCCG  
CTTCTGGCACTTCCGGCTGGAGGCCCTGTGTCAGTGGCAACAGATGATGGTGAGA  
TGATTTCGTGCAACAGCTGGCAATGGCTTCAATGGCATGTTCTCCGCTGCTGAAACCA  
AACGAAAGAGGGGATCAGTATGTTGAGGACTCCTTGACAGACCTCCGGCTTTTAAAC  
CCCCAACTGGCAGACCGGGATTACCTGAGGAGTCAGTGTGTGCACTTGTAGCCC  
CAAAGAACTGAGTTAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGCGCTGTGTTAATGGCGGGAGGTCAACAGTGTAGAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCAATTGTGTCAGAGAAATGAACCTTATTCACT  
TTTATCAGAGTTAAAGTTAACTGAGGGTTTATGGTCACTACATATTCAAGGCAAAA  
AAACTGCCCACAACTACAGAACAGCCTGTCACCAACCATCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTCAAGTGAACTTGTATTAGCGGCACTGTTATCACACCATCACTCGGATGGAGTTG  
CACGCCACAGTCTGATCATCAACATCTAACAGAGGAAATTTGGCAATTCAAGCGGG  
CAAGAACATGAGTGGCAGGCTGACTGTCCTGCAAGCAGTGCCTCTCCCTCAGAAGAGTC  
TAAATTACATTATTGGGCCAAGTAGGTGAGAAGATGGGGCAGGCAAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGGACCAAGAATCAAGAGCTCTGGATGCCCTTAAAGGAACTG  
TTAACAGTGAACCTGTCATTTAGCTGTATTCTGCCATTGCCATTGGAAAGATCTATGTT  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCTCCGAGATAGCTGAGGGAAAGTTCTT  
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAAACCTGCGACTTAGTGCCTGATAGGA  
AGCTAAAGTGTCAAGCGTTGAGCAGCTGGAGCGTTTATTTATACATCTGTAAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAGATGTCAAAAAAAGATTAGAAGTGTCAATATTATAGT  
GTATTGTGTTACCTCAAGCCTTGGCTGAGGTGTACAATCTTGTCTGGCTTTCTA  
AACTCAATGCTTAATAAAATTTTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLESNDLCRYDFDVYNGHANGQRIGRCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPERGDQYCGGLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFKEFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFFPVTTGLKPVALCQQKCRTGTLEGN  
YCSDSFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNOKLLDALKNKOC

#### **Signal sequence:**

amino acids 1-23

#### N-glycosylation site.

amino acids 355-359

### Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

#### Tyrosine kinase phosphorylation site.

amino acids 199-208

#### N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### Cell attachment sequence.

amino acids 149-153

## **FIGURE 39**

CGGACGGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCCTTCTT  
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGGTAAGAGATGGCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCTCAGCCTTCTCAACCTCCAGAACCTATCTGG  
CTCCAGCCCTCCACCTCCCCAGTCTTCCTCCCCGCTCAGGCCCATTGGTGCATAACCTG  
CCGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAAACCACCGGGACAACCTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAAGACAGTGAGACCCGCTG  
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCACCGCCTGCTGGAGCT  
GAGTGGAGAGCTGGTGGAGAGCTGGTTTACAAGCAGCAGGAGGCCGGACCTTCTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC  
CTTCCCTGTCTGGGGAAACAGAGGGCCCTGCGGTGGTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAACCGGCTACGGGGTGAGGCCGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCACGCCATCTGGTATGTTCGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTCGGTGAACACTGAGGGCTCTATGAGTGCAGACTGTGCCAAG  
GCCGCTTAGGCTGCATGGGGCAGGGCAGGTGCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTTGAGTGTGAGACAGAGGTGTGTCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATGTGTGAAGGAGCAGATCCAGACTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGCCA  
CGCTGGCTGCTAACGGCGACTGGTGTACCGCCATCTCATGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCCACCTGTAGGACCTCCTCCACCCACGCTGCCAGAGCTGGGCTGCC  
TCCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCCTCACAGGGTGGGGCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTTCTGT  
TCTGTGTTCACACATCCCCACCCCATGGCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAA

# **FIGURE 40**

MAPWPPKGGLVPAVLWGLSLFLNLPGPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLESEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCPGGTERPCGGYGCQCEGEGRGGSGHCDCQAG  
YGEACGQCGGLGYFEAERNASHLVCSACFGFCARCSGPPEESNCLQCKKGWALHHLKCVDIDE  
CCTEGANCAGDQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPEASAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCCTCTGCAGCCTTCTAAGGGACAGCCCCACTCTGCCCTTGCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCTGGCAGCCTGCTGCCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGGCCAGGGACCGCTCCCGGGAAAGAGGTTCAAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCTTGGAGGCCAGCACACACTGCTGGTGGCG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAAGGCCGTGCTGCCCTTCCAGG  
AGCCGGTCCCCAAGGCCCGCTGCACAGGCCACGGGCCGTGCTCCCCGCCAGGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTCGCGTCCCGACGACGGCTCCAACCGCACCTCCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGCTGGAAAGGCCCTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGGAGCCGCTGCTACAGGTGTCGGTCAAGAGG  
GAGCATCTGGGCCGCTGGCGTCCGCCAACAGCTGGTCCGCTTGCTCGAGGGGGC  
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG  
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGTGCTGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGCGAGAGAACTGGGTGCTGGAGCCCCGGCTT  
CCTGGCTTATGAGTGTGTTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC  
CGTTCTGGGCCCTGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCCTGGATGGTGCCTGCAAGGAGGCTCCAGCCATAGGCCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTTCTGAAGTGGTGCAGGGTACCGAGAGAGCTG  
GGCATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTAGTGAGGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTGGCTTCTCAGGAATGAGAAATTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTTATTCTTACTGCACTATATTCTAACGACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTGTCCTGTCAC  
TGGATCTGGCTAAAGCTCCACCACACTGGACCTAACGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAAAAGACTTGTAAAACATGAATAAAACACATTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEP  
VPAKAALHRHGRLSPRSARARVTVEWLVRVDDGSNRRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRRPRQPLLLQSVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTGTCACTGGCCTGATCCGGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCAATTGGCATCCTGTTGTGCTCCCTGG  
CATTGGGCACTGTTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTCTCCCCGTGTGGAGTGAAGTTGACCA  
AGGAGACACCACCAAGACTCGTTGCTATAAAACAAGATCACAGCTTCTATGAGGACCGGG  
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGCGGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCCATCCAAGCCTACAGTTAACATCCCTCTGCCACCATGGGAACCGGG  
CAGTGTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT  
GGGATAGTGATGCCATCGAACATCCAAAAGCACCGTGCCTCAGCAACTCTCCTATGCT  
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCCTGTGACGCTCTGATACTGGAGAACACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGTCTCGTGGCAGCCGCTTGTAACCCGTATTCTCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCATAGCGGAGGCCACTTGACAGAACAAAGAACGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCACCTAGTGCCTGAAGTGAAGGAGAACCAAACAG  
ACCTCGTCATCCCTGGTGATGCCTGGCTCAGGCTACCGCCTATCATCTGCATTGCTTACT  
CAGGTGCTACCGGACTCTGGCCCTGATGTCGTGAGTTACAGGATGCCATTGCTTC  
TACACCCACAGGGCCCCACTCTCGGATGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCATGCCCTCCCTTCCCTACACTGCTGAGTGGCCTGGAACTTGTAAA  
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTCCC  
TTCTAAGTAGACAGCAAAATGGGGGGTGCAGGAATCTGCACTCACTGCCACCTGGC  
TGGCAGGGATCTTGAGATGGTATCTTGAGCTGGTCTGGCTTCTTCTTGACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG  
TGATGACACTGGGTCTTCCATCTGGGCCACTCTTCTGCTTCCATGGGAAGTG  
CCACTGGGATCCCTGCCCCCTGCTTCTGAAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAATGGGAGCTTGTGAGAGCATAGTAAATTTCAGAGAACCTGAAGCAAAAG  
GATTTAAACCGCTGCTAAAGAAAAGAAAAGCTGGAGGCTGGCGCAGTGGCTACGCC  
TAATCCCAGAGGCTGAGGCAGGGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA  
ACATGGAGAACCCACTGGAAATACAAAGTTAGCCAGGATGGTGGTCATGCCGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAGAGCAAAACTCCAGCTAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLAGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGN SYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS  
SYVLNPTTGEVLVDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGTGTGGGACAGCTGAGCGGCGGTTGGATGGCGCAGGTTGGA  
CGCTGGCGAACAGGGCTCTGGGCTGGCGCTGCTGCTGCTCGCCTCGGACTAGGCCT  
GGAGGCCGCGAGCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGGCCAGCTAG  
GCTCGTGCACCCCACCAAGTCCAGTGCCGACCAGTGGCTTATGCGTGCCTCACCTGG  
CGCTCGACAGGGACTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACGCCCTGGCTCCCTGCCCTGCACCGGGCTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCACTGCAGGCCCTGGCTGCCCTAGCA  
GGCGAGCTCGGTGACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCAGGGCCA  
CCCAGACTGTCCCACCTCACCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG  
GGGATGCCAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGGAATGCCACATCTC  
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGGAATGCCACATCTC  
CTCTGCGGAGACCAGTCTGGAAGCCAAC TGCCATGGGTTATTGCACTGCTGCCCTG  
TCAGTGCAAGCCCTGGTCACCCACCCCTCCCTTGTGCTGGCTCCGAGGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGTCAGAACAGAAC  
CTCGCTGCCCTTGAGGACAAGGACTTGCCACCCGTCACTCAGGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGTGCGGATGGGTACCCGGCACCCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCGGGGAGCTAGGATGGGAACTGCCACAGCCAGAAC  
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLLLLLGLGLGLEAAASPLSTPTSAQAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLAACLAGELRCTLSDDCIPLTWRCGDGHPCPDSSDELGCGTNEILPEGDATTMGPV  
LESVTSLRNATTMGPVTLESPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSPL

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTCCGCACAGATGCGG  
GTTAGACTGGGGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTTCAGAGCAGCAGCAGCAGCACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAAGTGGCTGTGCTTCGCCCTGCACAGCTCACGGGCGGTT  
CGATGACCTTCAAGTGTGTGTGACCCGGATTCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAAGGCTCTGTAGCCCATTCACTGCCAACGAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAACTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCCGACCTACAAATATGTTTCAATTATGTCGGATGATGGAACGTGGAAATAATCTGCC  
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTCAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGGCTATCTGAGTGCTTACAAAACCTTATCTGGTGTCCAGGCCACCCGGTG  
CCTTGCTCTGGAAGCCCAACTCTGCCACTACCTCAATGGTAGTCACGGAGATTCTGTCT  
GCCACCCCGCCCTTGTGAGGCTACAACCAACGGAACTGTGGTGGAGTTTACTGCGATCCCT  
GGTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAAGATTGTGGCTCACGGCAACCAGTGTGCTGTGGTGTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG  
TTCCAGCAGTGCACCTGACTTTGTGGTGGTAGACGGCTGCCGTATGCTCCGTCTTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCTTAGGCCCCGGTACATGGCTCTGTGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGGACCGGA  
CACAGGCCAGGGAGTCAGAAAACCTGTGACAGCGTCTCAGGCTCTCTGAGCTGCTCCAAA  
GTCTGTATTCAACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTGGACAACCCCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAAGCCCAGGCATCCATGCCCCTGGGT  
GTTGTTCCAAGAAAACTGTGATTAAGGAAATTCCAAAGTGTCTGAAGTGTCTCTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCCTCTCTGGTTTAGACAAATGAAACAA  
AGCTCTGATCCTAAATGCTATGCTGATAGAGTGGTGGAGGCTGGAAAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTTAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGVFFEGSVARFHQCQDGFKLKAGTKRLCLKHFNGLTGWI PSDNSICVQEDCRI  
PQIEDAEIHAKTYRHGEKLIITCHEGFKIRYPDLHNMSLCLRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSPVGTVISYRCFPGFKLDSAYECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKITYTCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIAFTATSVLLVLLVILARMFQTKFAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDPGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACACGGTCCGCTCCGCCTCCCCCGCCTCCGTGCGTCCGTCGGTGGCTAGAGA  
TGCTGCTGCCCGGTTGCAAGTGTGCGCAGCCTCTGCCCGCCAGCCGCTCACCGCCGT  
AGCGCCGAGTGTCCCCGGCGACCCGAGTCGGGCCATGAGGCGGGAAACCGCGTACAGG  
CCGTGCTGCCGTGCTGGTGGCTGCGGGCTGCCGGCGACGGTCCGCTGAGTGC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCCTGTTA  
TAAAGTCATTACTCCATGATACTCTCGAAGACTGAACATTGAGGAAGCCAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAA  
AAGTTCATTGAAAAACCTCTGCCATCTGAGGGTGAATTGGGCTCAGGAGGCGTGA  
GGAGAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT  
ACAATTAGGAACATGGTATGGATGAGCGTCCTGCCAGCGAGGTCTGCGTGGTCATG  
TACCATGCCATCGGACCCCTGGCATCGAGGCCCTACATGTTCACTGGAATGATGA  
CCGGTGCACATGAAGAACATTGCAAATATTCTGATGAGAACACCAGCAGTCCCTT  
CTAGAGAACGCTGAAGGTGAGGAAACAGACTGACAACACTGTACTTCCAGAACACAG  
GAAGAACGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCC  
CCTAATCCCCAGCATTCCCTCTCCCTCTTGCTGCTCACACAGTTGATGTTGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCAGACCCCTAGCACAAAGAACACACCATC  
TGGCCCTCTCCTACCAGGGAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAA  
AACGCAAGACTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCTCCAGTGTT  
CGGGAGAACCCACTCCCGATGACATGCTTGTGACTATGACAACATGGCTGAAACCATCA  
GAAAGTGGGTTGTGACTCTGGTGGAGCTGGATTTGTGACCAATGACATTATGA  
GTTCTCCCAGACCAAAATGGGAGGACTAAGGACTCTGGATGGTGGAAATGAAATATG  
GTTATTAGGACATATAAAACTGAAACTGACAACATGAAAGAACATGATAAGAAA  
CTCTTATTTCTATAAGGAAAATACACAGAAGGTCTATGAAACAGCTTATGAGCT  
GGATGAGCATGTTGCCCCAGCACCTCTGGACCCCACTGGTGTATCCTTAT  
CCCAAGCCAGTCATCCAGCTGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA  
GAGTCCTCAATAATGTCATTGGTTGGTGTATCTAACTTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAGATGGGCTGGAGCTGGAAAACCACCTCTGTTCTGCTCTACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGGCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTCAAAGAAATAAAATCAA  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDDLRLGGQPVCRRGGTQRPCYKVIYFHDTSRRL  
NFEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAGEETELETPVLPTEETQEDAKKTFKESREAALNLAYILIPSIPLLLLLV  
VTIVVCWVWICRKRKREQPDPSKKQHTIWPSPHQGNSPLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLSVESGFVTNDIYEFSQDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCCTCGCAGCCTAACCGGAGGGCAGCGAGGGCCTACCACCAATGATCATGGTGT  
GTCAGCATGCCCTGTGGACCCCAGTGGCGCTCGACCTCGCTGGCTACTGCCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTCAGGTCTGTTCTGACACGGGGCTCGGAGTCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCACGAGACCAACCTGAAGGGGGCATGTTGCTGGCGACTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGCTTTATTGCTTCCACTAACATTTCGGAACTCG  
GAGTCCACCCGGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAAGACTGTTGATCCAAACTACCAAAGCTGCTGGAGGCTGA  
GGCAGAGAACGAGGCGGAGGCAGACTGCCCTTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTAGTATAAGTGGACTTCTTCATCTCCT  
GGACAACTGTTGGCTGGCAGCAGGACACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCCCTCATGATG  
TGACCTTCATACCGCTTAATGACCCCTGGGATTTGACCAAAATGGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAAGCTCTA  
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCAGAAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRRQTAISLQPGISEDLKKVKDRMGIDSSDKVD  
FFIILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES  
NLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTAACATACTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGCAACCAGACCTGGATTCCCTAGCGCTCCATCTGGAGTCGGCCTGGTGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACCTGGCTGTGTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGGGTATTGGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGCATTGCAAGGGACCGTGGAAAGTGA  
GCACCAAGAACCATGGTATACCGTGTGCCAGACAGGCTGGAGCCCTCCGGCGAAAGGTGG  
TGTGCGGCAGCTGGATGGGAGGGCTGTACTGACTCAAAACGCTGAAACAGCATGCC  
TATGGCCAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA  
GGATTGCCCTCTGGGCCTTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTGTG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCACTG  
GAGGTGCTGCAACAGGGCTATGGGCTCTGTGATGACAACCTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGGTGTGCCGATCTGGCTGGATAATGTTGCTCAGGGGAGGAG  
CAGTCCCTGGACAGTGCACAGATTTGGGGTTTACGACTGCACCCACCAGGAAGA  
TGTGGCTGTATCTGCTCAGTGTAGGGGCATCATCTAATCTGTTGAGTGCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTCTGCCCTGGACTGGGACTTATACTTGGTCCCCCTGATTCTCAGGCCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACTACATCA  
CCACCTTCCTATGTCCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCAATTGTCCTGTTCTGAGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAAATTCTGAAATTGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGTAACCTTATTACAATAATAAGATAGCAC  
TATGTGTTAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQGTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGC GKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTATCGATTGAATTCCCCGGGGATCCCTAGAGATCCCTCGACCTCGAC  
CCACCGTCCGGACCGTGGCGGACCGGTGGGCCGCTACCAGGAAGAGTCGCGAAG  
GTGAAGGCCATGGACTTCATCACCTCACGCCATCCTGCCCTGCTGTTGGCTGCCTGGG  
CGTCTCGGCCCTTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCTACCTCGGAATGCTG  
TGGTGGTATCACAGGCGCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTATGCT  
GCGGGTGCTAACTGGTGCTGTGGCGGAATGGTGGGCCCTAGAACAGCTCATCAGAGA  
ACTTACCGCTTCTATGCCACCAAGGTGCAAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGA  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTTAACGAAAGCACTCC  
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCTGCGTGGCGAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGTACA  
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACACACACAGCCAGGGCCGAAGCCCTGTTGGAGGTGGCCAGGATGTTCTGCTGCTGGG  
GAAGAAGAAGAAGATGTGATCCTGGCTACTTACTGCCTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCACTTTAGGTTGC  
TTACTCTACAAGGGACAGTTGCATTTGAGACTTAATGGAGATTGCTCACAAGTGGG  
AAAGACTGAAGAAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTTCCCAGGGTGGAGGGAAACACTTAAGGAATAAATGGAGCTGGGTTAACACT  
AAAAAACTAGAAATAAACATCTAAACAGTAAAAAAAAAAAGGGCGGCCGACTCTAG  
AGTCGACCTGAGAAGCTGGCCGCCATGGCCCAACTTGTGTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAABILQCFGYVDIL  
VNNA  
GAGISYRGTM  
DTTV  
DVKRVMETNYFGPV  
VALTKALLPSMI  
KRRQGHIV  
AISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVT  
VISPGYI  
HTNLSVNA  
ITADGSRYGV  
MDTTT  
AQGRSP  
VEVAQDV  
LA  
AVGKKKD  
VILAD  
LLPSL  
AVYLRT  
LAPGLFF  
SLMASR  
ARKER  
KSNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

CCACCGCGTCCGCTGGTAGATCGAGCAACCCCTAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAAACACACCAAACGCTCGCAGGCCAAAAGGGATGAAATTCTCTGGACATCCTC  
CTGCTCTCCGTTACTGATCGTCTGCCAGAGTCCTCGTAAGCTTTTATTCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTCTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTGCTAAACTAAAGCAAGCTGGTTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTTCATACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATAATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTAATGCACTTGACATTTCTGGACTACAAA  
GGCATTTCCTCCTGCAATGACGAAGAATAACCATGGCCATTGTCACTGTGGCTTCCGCAG  
CTGGACATGTCCTGGTCCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGGGA  
TTTCATAAAAACCTTGACAGATGAACTGGCTCCTACAAATAACTGGAGTCAAACACATG  
TCGTGTCCTAATTGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGGACCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGTTTTAACACATTGGAAAGGATCCTCTGAGCGTT  
CCTGGCAGTTTAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAAAGCACCTAGTTCTGAAAAGTGAATTACCCAGGTTAGGTTGATGTCATCTA  
ATAGTGCAGAATTAAATGTTGAACCTCTGTTTCTAATTATCCCATTCTCAATA  
TCATTTTGAGGCTTGGCAGTCCTCATTACTACCACTGTTAGCCAAAGCTGATT  
ACATATGATATAACAGAGAAAACCTTACGGTGAACCTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAAATAATTCCAAGATTGTTGAGCTCACCTGAAGGCTTGCAA  
AATTGTAACATAACCGTTTATTAAACATATTTTATTGATTGACTTAAATTGTTG  
ATAATTGTTGTTCTTTCTGTTCTACATAAAACAGAAAATCAAGCTCTAAATAAAA  
TGAAGGACTATATCTAGGGTATTTCACAAATGAAATATCATGAACTCTCAATGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCAATGCCAAACATTCT  
GCACAGGGAGCTAGAGGTGATAACCTGTTGCAAGTATAAGCATCACTGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA  
AAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 58**

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSI  
LVNNAGVV  
YTSDLFATQDPQIEKTFEVNLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC  
SSKFAAVGFHKTLTDEAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVINGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCACCGCGTCCGGGACCGCGTGGGTGACTAGTTCTAGATCGCAGCGGCCGCCGGCTC  
AGGGAGGAGCACCGACTGC CGCCGACCCCTGAGAGATGCTGGTGCCTATGGAAGGTGATTG  
TTTCGCTGGTCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCTCCCTATACAGAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGGAAAGGAATTGAGAATTTGAGCTGGGACATGGGGCTTACGGACTGAACATGA  
AGAGTTATGCCGGCTTCTCACCGTGAATAAGACTTACAACAGAACCTCTTCTGGTT  
TCCCCAGCTCAGATAACAGCAGAAGATGCCAGTAGTCTCTGGCTACAGGGTGGGCCGG  
AGGTTCATCCATGGACTCTTGAGGACATGGGGCTTATGTTGTCAAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCCTGGACCACAAACGCTCCATGCTTACATTGACATCCA  
GTGGGCACAGGCTTCAGTTTACTGTGATGCCACCGGATATGCACTGAGCTCAATGAGGACGATGT  
AGCACGGGATTATAACGTGCACTAATTCACTGTTTCCAGATATTCTGAATATAAAAATA  
ATGACTTTATGTCAGTGGGAGCTTATGCACTGGGGAAATATGTCAGGCCATTGACACCTC  
ATCCCATTCCCTCACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGAGAATTCTGTACCAAATTGGCT  
TGTGGATGAGAAGAAAAAAAGTACTCCAGAAGGACTGCCATGAATGAGAACA  
AGGAAGCAGAACACTGGTTGAGGGCTTGAATTAACCTGGATAAAACTACTAGATGGCAGCTTAAC  
AAAGTGATCCTTCACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGCCTG  
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA  
GCCATCCACGGGGAAATGAGCTTAACTGGAAACTATAGTGGAAAAGTACTTGGAGA  
AGATAACGTACAGTCAGTTAACGCCATGGTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACATGGCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTTGATGGC  
ATGGACTGGAAAGGATCCCGAAATACAAGAAGGGCAGAAAAAAAGTTGGAAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCCGCAAGCGGGTAGCTTCCATCAGGAATTATT  
GAGGGTGGAGGACATATTTCACCCATGACCCAGCTCTGAGAGCTTGTGACATGATTAACTCGA  
TTCATTATGGAAAAGGATGGGATCTTATGTTGGATAAAACTACCTTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTGAAACAAAGTGAGC  
TTTTGTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA  
TTATTTAACCTAAAGGATGAAAGGTATGGATGATGTCACACTGAGACAAAGATGTATAATGA  
AATTGGGTCTTGAATAGGAAGTTTAATTCTCTAGAGTAAGTGAAAAGTGCACTTG  
TAACAAACAAAGCTGAAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTTGGAAAATATTGATGAGAATAGCTCAATTATCCAAATAATGGATGAGCTATAA  
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGCTTGAACAAAAGAATTCTTGAATAA  
AAAATATTATATAAAAAGTAAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGCPDGLFRSLYRSVSMPKGDSGQPLFLTPYEAGKIQKGREL  
VGPFPGLNMKSAYAGFLTVNKTYNSNLFFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEEDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKKQYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDGLTSDPSYFQNV  
CSNYYNFRLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTTIVEKYLREDTVQSVPWLT  
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYI  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTCGGCTCGGAATGGCACATGGGAACTTCCAGTCTTGTGGCTACAAACAT  
TTTCCCTTCTAACAGTCTAACAGCTTCAACAGCTAGTGTACAGGGGTTCTTCTT  
GCTGGAGAAGAAAAGGGCTGGGGCAGAGCAGGGCACTCTCACTCAGGTGACCAGCTCC  
CTCTCTGTGATAACAGAGCATGAGAAAGTGAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAATAGGAAGGAATTCTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCTGCTAACACGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT  
AAGACGTGCGGTAGGATAGGAAGACTGGTTAGTCTTAATCAAATTGACTGGCTGG  
TGAACCTCAACAGCCCTTTAACCTCTCTGGAGATGAAACGATGCTTAAGGGCCAGAAA  
TAGAGATGCTTGTAAATAAAATTAAAAAAAGCAAGTATTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCTGAAACATTCTAACAGGGAGAAAGTATGTTAAATA  
GAAAAACCAAATGAGCAGAAGGGAGACTCACAGAGCTAACAGGAGATGGGACCTGGTC  
AGGCCAGCCTCTTGCCTCCCGGAAATTATTTGCTGACCAACTCTGCTTGTGTTT  
GCAAAATCATGTGAGGGCCAACGGGGAAAGCTGGAGCAGATGAGCACACACAGGAGCCGCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCCAGCTCTGTGCTCTGCTCATGAGCTGGCTCTGGCCCTGGAGGTGGCAGCCGC  
ATGCCCTAGTTCAGCACCTTCACTCTGAGAACATCGTACGGACCTTCAACCAACTTGACCGT  
CCACCAAGGGACGGGGCCGCTATGTGGGGCATAACCGGGCTATAAGCTGACAGGCA  
ACCTGAGCATCAGGGCTGCTCATAAAGACAGGGCAGAACAGGACAACAAAGTCTGTTACCG  
CCCTCATCGTGAGGGCTGAGGAGCTCCACCTACCAAAATGTCACAAAGCTGCT  
CATCATGACTACTCTGAGAACGGCCCTGGCCCTGTGGAGCCCTACCCAGGGGCTGTGCA  
AGCTGCTGGGCTGGATGACCTCTTCATCTGGTGGAGCATCCCAAAGAAGGAGCACTAC  
CTGTCAGTGTCAAAAGACGGGACCATGACGGGGTATTGTGCGCTCTGAGGGTGAGGA  
TGGAAGCTCTCATGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCCGACCCCTGTCCA  
GCCGGAAAGCTGCCCGAGACCTCTGAGCTCTGAGCATGCTGACTATGAGCTACACAGC  
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGCTCTCCAAATTGACAT  
CTCTACATCTACGGCTTGTGAGTGGGGCTTGTCTACTTCTACTGTGTCAGCCGGAGA  
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTCATCACCTCACGCGATGTGCG  
CTCTGAAGGATGACCCCAAGTCCACTCATACGTGTCCTCGCCCTTGGCTGACCCGGC  
CGGGGTGGAAATACCGGCTCTGGAGGCTGACGGCTGTTACCTGGCCAAGCCTGGGACTC  
AGGGCTTCAATATCACCAGGCCAGACGATGACTCTGCCCTGTGTCCTCCATCGGGCC  
CACTGAGTACCAACCCGCCGATGACTCTGCCCTGTGTCACCCAGGGAGGGCAACCTGGAG  
GCAGATCAAGGAGGCCCTGAGCTCCAGTCCAGGAGGCCCTGTGTCACCCAGGGAGGG  
TGCTGGGGAGGAGCTCCAGTCCAGGAGGCCCTGTGTCACCCAGGGAGGGCAACCTGGAG  
CTGGGACATCAACCAAGGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTAC  
CAGCAGGGACCCGATGACCTCTGTGAGGCTTACAGGCTACAGCGTGGTTTTG  
TGGGAGCTAAGAGTGGCAAGGCTGAAAAAAGGTAAGAGTCTATGAGTTCAAGTCTCC  
ATTCACTTCTCAGCAAAAGAGCTCTGGAGGTAGCTATTGAGGAGATTAACTATAG  
GCAACTTATTTCTGGGAAACAAAGGTGAATGGGAGGTAGAAGAAGGGTTAATTG  
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCACTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCTAACCTTAAGAAAAACTTAAAGAAGGTACATGCAAAAGCAA

## **FIGURE 62**

MGTLGGQASLFAPPGNWFWSDHSAALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSDRSVVLSSVVWLLAPPAAGMPQFSTFHSENRDWTFNHLTvhQGTGAVYVGAINRV  
YKLGTGNTLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL  
YQGVCKLRLDDFLILVEPSHKKEHYLSSVNKTGTMGYGVIVRSEGEGDKLFIGTAVDGKQDY  
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFAASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFIAFSKGQKQYHHPPDDDSALCAFPIRAINLQIKERLQSCYQGEGN  
LELNWLGLGDVQCTKAPVPIDDNFCGLDINQPLGGSTPV EGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGGGACTGGGACTGGGAAACCGGGTCCCGCGCTTAGAGAACACCGCATGACCA  
CGTGGAGCCTCGGGGGAGCGGGCCGACGCTGGGACTCCCTGCTGCTGTCTGGGCTTCCTGGCTCC  
GCAGGGCTGAGCTGGAGCACCTGGCTCCCTGCCATCGGACTCCGGGCTCCATCGAACAGCTGGGGCTGCAGGGCAAGGGCTGGA  
ACTTCATGCTGAGGAACTCCATCTGGATCTTCGGGGCTCCATCGGACTATTCCTGGTGTGCCCAGGGAGTACT  
GGAGGGACCGCTGCTGAAGATGAAGGCTGTGGCTGACACCCCTCACACCATATGGTTCGGTGAACCTGCTAG  
AGCCAGAAGAGGCAAATTGACTCTCTGGGAACTTGGGACCTGGAGGGCTTCGCTCTGATGGCCGAGAGATCG  
GGCTGTGGGTATTCTGGCTCAGGCCCTACATCTGCACTQAGATGGACCTCGGGGCTTGCCCCAGCTGGCTAC  
TCCAAGACGCTGGGATGAGGCTGAGACAACCTAACAGGCTTCAGGAGGCTTCAGGAGCAGTGGACCTTTATTGACCACC  
TGATGTCTCAGGGTGTGCACCTCAGGATACAAGCTGGGGGACCTATACATGCCGTGCAAGGGTGGAGAAATGAATATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGCTAACAGAACGACTGGAGGACCGTGCATITGTAACGTC  
TCTCAGACTCAGGACAAAGGATGGCTGAGGAGGATTCTGGAGGACTTGGGACACCATCACACTTGCAACT  
CAACACAGCAGCTGAGCTTCTGACCTTCTCTCAACGCTCAGGGACTCAGCCAAAGATGGTGTGAGTGGAGT  
ACTGGAGGGGGTTTGTGACTCTGGGAGGCCCTCAAAATCTCTGGATTCTCTGGGTTTGTGAAACCGTGT  
CTGCCATGTGGAGGCCCTCTCCATCAACCTCTACATGTCAGATGTCACAGCTGATGCTGCTGATGAGAACGGCG  
GAGCATGCACTTCATGACTACAAAGTCAAGCTGAGGACCTTCAGGAGGACCAACTTGGCTTCATGAATG  
ATTACACGGGAGGACTACATGAAGGCTCGAGGACTCTGGGCTCATCTCAGGACATCCCTCCCGGACACCTG  
ACCTCTTCCCAAGGACTGGCTTATGAGGCTTAAACCCACTCTGACTCTGACTCTGCTCTGGGACCCCTCAAGTAC  
TGGGGGAGGACTCAAGTCTGAAAAGGCCCAATCAAGGAGAACCTGGGAGCTGGGAGGAAATGGACAGTCT  
TCGGGAGACATCTCTGAGACAGCATCCTCTGCTGCTGCACTTCTGAGGACCTGGGACCTGGGAGG  
TGTTTGAGACACAGTATCCA TAGGATTCTGGACTACAGAACAGAAAGATTGCTGTCCTCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCTGGGAGCTGAGCAACTTGGGAGGAAATTTGATGACCGAGCCAAAG  
GCTTAATTGGAAATCTCTATCTGATGATTGATTCCACCTCTGAAAAACTTCAGAATCTATGACCTGATGAAAGA  
GCTCTCTTCAAGGAGGCTGGCTCTGGGACAAATGGNGTCTCCCTCCAGAAACACCCACATTACCTGCTTCTCTGG  
TAGCTGTGCTCATGCTTCCACGCTTCCACGCTTCTGACACCTTCTGAGGCTGGAGGCTGGGAGGAGGGGGTTGTATTCA  
TCATGCGGAGGAACTTGGAGGTTA CTGGGACATCTGGGACAGGAGACGCTTACCTCCAGGCTCTGGTGA  
GCAGGGAAATCAACCAAGGACTCTGTTGGAGGAGCATGGGGGGCTCTGACATTACAGTCAAGGAAACCCCC  
ACCTGGGAGGAACTGAGTCAAGCTGGGAGTGGCACCCTCTCTGCTGCTGGAGACTGGGAGACTGGGCTC  
CTCTGACCTGAAAGCTGGCTGGCTGCTGCCCTCCACCTGCAAAAGCATCTCTTAAGGAGACCTCCTCAGGG  
ACTGGGAGGACTCAAGTCTGCCCTGTCTGAGCTAACCTGAGGGAAAGGTGGATGGCTCTGGG  
TGCTTCTGGTGTGATGATGCTTCTACAGGCCCTGCTCTGCTGCTGAGGCTGTCGGGCTGCTCTAGGGTGGGAGC  
AGGAAATCTGAGATGCCAGGCTTGGGCTCAGGAAAGGGGAGGCTGCAAAAGCTGCCCTTGCACGGGAGCTCACAGGCC  
TGCAGGACATCTGCTGAGCTCAGGGCTGCTCTTCTGTTCTGGGAGGCTTGGGACATCTCTCATGGG  
TTTATCCCGAAATCTGGTGTGCTCAGGAGTGTAGAGGGTGGGAAAGGGGTGCTCTCACCTGAGCTGACTTTGT  
CTTCTCTCAACACCTCTGAGGCTTCTTGGGAGATTCTGGGAGGACTCTGGGCTGAGAACACATGTGACTTCCCT  
TCCCTTCCACCTGCTGCTCTCCACAGGGTGACAGGCTGGGCTGGAGAACAGAAATCTCACCCTGCGCTTCT  
CAAGTTAGCAGGTGTCTCTGGTGTCACTGAGGAGGAGCATGTGAGTCTGGCAGAGGACATGGCCCATGTCTGCA  
CATCCAGGGAGGAGGAGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAGGACATGGCCCATGTCTGCA  
AGGGAGGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAGGACATGGCCCATGTCTGCA  
GGGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAGGACATGGCCCATGTCTGCA  
ACAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAGGACATGGCCCATGTCTGCA  
GAAGTGTGTCAGTCCAGTCCGCAATTGAGGCTTGTGGGGCCAGGCCAACACTGGCTTGGGCTACTGTCTG  
GTTGAGCTAAAGCTATAACCTTGAACAA

## **FIGURE 64**

MTTWSLRRRPARTLGLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYWPWNLHPERGKFDFSGGNLDLEAFVLM  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVIDLYFDHLMMSRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAVMPYVKKALEDRGIVELLLTSNDKGLSKGIVQGVLAT  
INLQSTHELQLTTFLFNVQGTQPKMVMEYWTGWFDSWGGPHNILDSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGNGQSFGYIYL  
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQGYTVLRLVENGRVNNGEN  
IDDQRKGLIGNLYLNDSPLKNFRIYSLDMKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## FIGURE 65

GGGGACGCGGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGAGGGTGGACGGGTCGGAGACC  
CTGTGAGGGTCTCTACTTGGCTTCGGGGTCAAGACGCAGCACCTACGCCAAGG  
GGAGCAAAGCCGGCTCGGCCAGGCCCCCAGGACCTCCATCTCCCATCTGGAGGAATC  
CCACACGTAGCGGTCTGCCGCCCTCAAGACTAGAGGAGCCTGAAACGCCATGGCTCCC  
AAGAACGCTCTCCCTCGTCTCGTACTGGATAGGGTCACTGCCCTGACGCTACTGCTGCCCA  
GCAGACACTCGGTCTCGTACTGGATAGGGTCACTGCCCTGACGCTACTGCTGCCCA  
CGTCCGCTATGTGTCGGCAGCCTGACTACTTCGGTACCGCGGGTCTGGCCGAC  
CGGCTTTGAAGATGGCATGGCCCTAACGCCATACAGTTTATGTGCCCTGAACTA  
CACAGGCCACAGCTGGGTCTATAACTTTAATGCCGGGGACCTCATTGCCCTCTGA  
ATGAGGAGCTAGCGAACCTGTTGGTCAACTGAGACAGGACCTACATCTGCGAG  
TGGGAGATGGGGGCTCCCATCTGGTCTCGAAACCTGAAATTCTACAGAACCTC  
AGATCCAGACTCCTTGCCTGGCAGTGAGCTCTGGTCAAGGTCTGGCCAAAGATATAC  
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGGTGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTCAGCTACATGAGGCACTGGCTGGCTCTCGTCACTGCTAGG  
AGAAAAGATCTGCTTCCACACAGATGGCCCTGAAGACTAACGTGTTGCCCTCCGGG  
GACTCTAACCTACTGTAGATTGGCCACAGTACACATGACCAACATGACCAAAATCTTACCCCTGCTT  
CGGAAGTATGAACCCCAGGGCATTGGTAACACTGACTACTACACAGGCTGCTGGATTAA  
CTGGGGCCAGAAATCACTCCACAGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGGCCAGTGTGAAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTCCCGATAAGAAGGGACCTCTCCGATTACTACAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAACGTTTGTCTTCGAGATGTCACTGAG  
TCCAGGAAGTCTTGGGACCTTACCTCCGGAGCCCAAGATGATGCTGGACCTG  
ACTCTGCACTGGTCTGGGATTACTGCTTCCCTGAGACTGCTTGGCCCGTGGGGCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAGCAGGACCATGGCTCATGTTGAC  
GAACCTATATGACCCATACCAATTGGGATGGGCTGTCAGGCTGACAAATATGGAGTC  
CATGACCCCTGCTATGGTATGGTGGGATGGGCTGTCAGGCTGAGGAAATATGAG  
AGACAAACTATTGGACGGGAAACTGGGCTCAAACATTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGTCAACAGCAGTACTCAAGGGCTGTTGAAGGCCAACATTG  
GGCAACAAACTCTTACCCAGTGGGATGATGTTCCCTGAAAGATTGATAACCTTGAGTG  
GTGGTTTCCCCTCAGTGGCAAAATGGCCATATCTCAAGCTCTCTGGCCCCACATTCT  
ACTCCAAAACATTCAATTGGCTCAGTGGGACACATTCTATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGGATCAATTGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGCC  
ACAAACAGACCCCTCACTGCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATTAA  
CATTGCTGAAACTAGAAGATGTACCTCTCAGGCCAAGTCATTTGGATAAGCTATC  
CTCAATAGCACTAGTACTTGGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAAACCAATTGGAGTTAAGTGGGCACTGAAGTAGGCCAGTGGGCTCATGC  
CTGTAATCCCACTTGGAGGCTGAGAGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCAACATGGTAAACCCCGTCCACTAAAAAATACAAAATTAGCGGGCTG  
ATGGTGGGACCTCTAACTCCAGCTACTTGGGAGGCTGAGGGCAGGAGATTGCTTGAATCC  
AGGAGGAGGGTGCAGTGAGTGGAGGTTGACACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWGLNATIQFYVPWNHYEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQGNHSTRSVSAVTKGLENMLKLGA\$VNMYMFHGGTNF  
GYWNGADKKGRFLPITT\$YD\$YDAPISEAGDPTPKLFALRDVVISKFQEVLGPLPPSPKMML  
GPVTLHLVGHLAFLDLLCPRGPPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVGDGVFQGVVERNRDKLFLTGKLSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQWINGFNLGRYWTKQGPQQTLVYVPRFLFFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCCTTGAAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAGCTCTCATCAGTTACATATCCATTATTGTGT  
TTATGGCTTATCTGCCCTCACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT  
CTTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAACGATTT  
GCGTTCCTCTTCACATGGTAGACCAGTATGACCAGCTATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGGTTAGTGAAGAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAAACTCAGGCAGCACATTCACGCAACCCCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAACCT  
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCAAGAGCTTCAACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA  
TGCCCTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCTGGGTGTTGCTCAAAAA  
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AACTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATTTACAAGTTAGTCAATTCTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCTTAAGAAAATGATGAATGTCGCTGAGCTGAACTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACTGGAT  
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTCCAGCATTAAACGACT  
GACTTGTAAAATTATGGCATACAAAATTGTTACTATTCCCTCTATTACCCATGTCA  
AAAACCTGGAGTCACTTTATTCTCTAACACAAAGCTGAATCCTTACAGTGGCAGTATT  
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTAACACAACTTCAATGATTCCAATAGA  
AAATTAGGATTGCTTCAGAACCTGCACTGGGAGCTTGAATCTGGACAGAACTGCATCACC  
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCAGCTGGGAGCTGTCGATGCTCAAGAAAAGCGGGCTTGTG  
TGAAGATCACCTTTGATACCTGCCACTCGAAGTCAGGACATTGAATCAAGACATA  
AAATTCCCTTGCAAATGGATTTAAACTAAGATAATATGACAGTGTGCAAGGAAC  
AACTTCCTAGATTGCAAGTGCACGTACAAGTTTACAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAACAGAGAGGATGCATAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTTAGGGTTTAAGTCATTCAATTCCAAATCATTGTTCTTTGGGG  
AAAGGGAAAGGAAAATTATAACTAAATCTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAATTGCTGCCGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAVMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDF AFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG  
VPDAVFDTLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLQELRLRHLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTLVLLVLSLKKMMNVAELELQNCELERIPHAFISLSNLQELDLKS  
NNIRTIEIIISFQHLKRLLTCLWLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNSIMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITS LP  
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRM LKSGL VVEDHLFD TLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCCCACCGCTCCGGGCTTCTCTGGACTTTGATTTCAATTCTTCATTGACAAACTGACTTTTATTTCT  
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGGCGCCCTGGGAAGACATTGTGTTTACACACATAAAGGAT  
CTGTTGGGGGGTTCTCTCTCCCTGGCATCTGGCATCTGGCTTGTGGTTGTGGGGGGGGAGACCACTGG  
GCTCAGTGCTGCTGCACTATTCTGCTTAGCTACATCGAAGTCTTGTGACCTCCATACAGTATTATGCTGTC  
ATCCGCTGGTGTATCTCGGCAGCTGGCTCTGCTGTGATAGTTGTGCTGCTGTCTTACTTCAAATAACACAAAC  
GGCTTAAAGCTGCAAAGGAACTGAAAGCTGGCTGTGCTGTGAAAAAAATCACACCCAGACAAGGTGCGCCAAAG  
AACAGCAGGCAAACCATGCCCCAGAGCTTGTCTGCTGCTGCTGAGGTGAAAGGATATAGAATGTGCGC  
AGTTTGATTCCCTGGCCACCTTGTGCTGTTGCTGAGTTAGGAAAGGCTCCCTTCTCAAA  
GCAGAGCCCCTGAAGACTTCATGATGTCATGAGGCCACCTGTGATGTCAGGCCAGAAAGAACAG  
CTCCCCATCAGTTCTCATGAAAATAACTCAGTGGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCCCTCAGGAAGGAGTTGGGGAGAGAACCCTCACTGTGGGAATGCTGATAAACAGTCA  
CACAGCTGCTCATTTCTCACACAAATCACCCCTGGCTGGCAACTGACCTTCTCCTGGAGGTGTCAGAAA  
GCTGATGAAACAGAGCTGGCTTAAGGCTGCTTCAAGGCTGCCAGGCCCTTGGCCAAAATGGAGCTGTA  
AGAAGGCTCATGCCATTGACCCCTCTAATTCTCTCTGTTGGCGGAGCTGACAAATGCGGAGGCTGAAGGCAAT  
GCAAGCTGACAGCTGAGTTGGGGCTGCAAAATGCGAGAGACCCAAAGGCCATGATCTGCAACTCAATCC  
AGTGAAGACTGACCCATTGACAAATAGAACAGCAAAACAAAGCATCAGATTCTTCTCATGTCAGCTT  
GATCCAGATGGAAGCTGAAAGTGAACACATTAAAGCTTGTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG  
CAAGTCTGAGATAAAAGCAGTATGTTGATCATCATCGATCATGGACCTTCAAATAGTAAATAGTAACT  
GACTCTGAGAAATTCAGAAGACTGCTTGTCTTCACTACTCTCTCTCTCATACATCTTCAACATCTTCAAACTG  
GGCGGTTACCTGGATCTGGCAACAGGCCAAATACCCAAAGGCCATCTGGAGCTGCTTCAAGGCTT  
TGTTGTTGGCACATACAAAGTGGAGAAATCAAGATCAAATAAAACTCAACATTCTCAAGGATTTTCTAGAAATAGAC  
AAACAGTGCACAAATTGATTTCTGCCATCTATGATGGCCCTTCCACCAACTCTGGCTGATTTGACAAGCTGT  
GGCGGTGACTTCCACCTGGCATGTCATCAAAACTCTGACTCTGGTTGTCTACAGGATATTGCAAACTT  
TACCGGGGTTCTGCTTCTACACCCATTAATGCGAAAATAACATCACACTACATCTTAACTGCTCTT  
GACAGGATGAGAGTTATAAGCAAATCCACCTAGAGGCTTTAACTTAATGGGAAATAACTTGCAACTAAA  
GACCCAACTTGGCGACCAAATAATCACAAATGTTGGAAATTCTGTCCTCTTAAATGATGTTGACAACTCAGA  
AAAGTGAAGATCAGTAATFACTACACCAATAATCACCTTCTGCACTCTCAACTTGTGAGTGATCACC  
CGTCAGAAACACTCCAGATTATGGAAGCTGTGAAATGGGACATAAATTCTACAGTGGAGATAATACATAACCA  
GAAGATGATGTAATCAAAGTCAAATCAGTGGCAATAATAACACAGCATGGCTCTTTGAACTCAATTCA  
TTGAAAAGGATATACTGGATCACATTATGTTGATTTGAAACCAACTTTTGTCAAGGTTAGCTGAC  
ACCTCAGATCCAATTGGTGTGTTCTGATACCTGTAGAGCCTCTCCACCTCTGACTTCTGCACTCTCAAC  
TAGGACCTTAACAGAGTGGATGTGAGGAGATGAAACTTGTAAAGGTGATACCTTATTGGGACACTATGGGAGA  
TTCCAGTTAATGCTTAAATTCTGAGAAGTATGAGCTTGCTGAGTTGATATGTTGAGTTGATATGTGAT  
AGCAGTGACCAACAGTCTGCTGCACTCAAGGTTGTGCTCCAGAGAACGAAACAGACATTCTCATATAAATGG  
AAAACAGATTCCCATAGGACCCATTCTGCTGAAAGGGATGGAAGTGCACAGTGGCAATTGGGATTCAGCAT  
GAACACATGGGAAAGAACATCCAACAGCTTCTGCACTGTCATCTGTTCTCATGTTCTAGCTCTG  
AATGTGTTGACTGTAGGGACAAATCACAGTGGGAGATTGTAATCACAGGGCAGACTACAAATAGGAAAGCTG  
CAAGACTTAACTAACAGGTCACCCCTAAGTGAGACATGTTCTCAGGATGCCAAAGGAAATGTCACCTCGT  
GGCTACACATATTATGATAATGAGGAAGGGCTGAAAGTGACACACAGGCTGATGAAAAAA

# **FIGURE 70**

MELVRRLLMPLTLLLISCLAEI TMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ER PENKSIRIIIFSVQLDPDGSCESENIVKVDGTSSNGP LLLGQVCSKN DYVPFESSS STLTF  
FQIVTDSARIQRTVFVFFYFPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSAS YTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTMNITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVVIQSQN ALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYD LIKGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSVVYL  
QCKVLI CDSSDHQSRCNQGCVSRSKRD ISSYKWKTD SII GPIRLKRDRSASGNSGFQHETHA  
EETPNQP FN SVHL F S FM VL AL NVV TVAT IT VRHFVNQRADY KYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAAGAACAGCGCTCCGAGGCCGGGGAGCCTGCAGAGAGGACAGCCGGCTGGCCGG  
GGACATGCGGCCCGAGAGCTCCCAGGCTCGCTTCCCGTGTGCTGTTGCTGTC  
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCCTGCACCCACCTGGGAGTC  
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAGTTCGGCATCTTCATCACTG  
GGGAGTGTTCCTCGCTGCCACCTCGTAGCGAGTGGTTCTGCTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAATTATGAAAGATAATTACCTCTCTAGTTCAAAATATGAAGAT  
TTTGGACCACTATTTACAGCAAATTTTTAATGCCAACAGTGGGAGATATTTCAGGC  
CTCTGGTCCCAAATCACATTGCTTAACCTCCAAACATCATGAGGGCTTACCTTGTGGGGT  
CAGAATATTCTGGAACTGGAATGCCATAGATGGGGCCAAGAGGGACATTGTCAGGAA  
CTTGAGGTAGCCATTAGGAAACGAACACTGACCTGCGTTGGACTGTACTATTCCCTTTG  
ATGGTTTCATCGCTTCCCTGAGGATGAATCCAGTTCTGCCATAAGCGCAATTCCAG  
TTTCTAAGACATTTCCGAGGCTCTAGTGTAGTGAAACACTATCAGGCTTGAGGTTCTGTGG  
TCGGATGTCAGCGAGGAGCACCGGATCAATAGTGAAACGACAGGCTTCTGGCCTGGT  
ATATAATGAAAGGCCAGTCGGGGCACAGTAGTCACCAATGATGTTGGGAGCTGGTAGCA  
TCGTAGTCAGCTGGTGGCTTACCTGCACTGATGTTATAACCCAGGACATTTTGCA  
CATAATTGGAAAATCTGCAATGACAATAGACAAACTGTCCTGGGCTATAAGGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAAGATTGGTAGACAAGCAACTTGTAGAGACAGTTCTATG  
GAGGAATCTTTGATGAATATTGGGCCAACACTAGATGGCAGCATTCTGTAGTTTTGAG  
GAGCGACTGAGGCAACTGGGCTCTGGCTAAAGTCATGGAGAACGCTTTTATGAAACCTA  
TACCTGGCGATCCCCAGAAATGACACTGTCACCCAGATGTGGTACACATCCAAGCTAAAG  
AAAAATTAGTCTATGCCATTCTTCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCAAAGCTTCTGGGGCACAGAGGTGAACACTTGCCCATGGACAGCCACTAATG  
GATTCTTGGAGCAAATGGCATTATGGTAGAACTTGCCACAGCTAACCATCAGATGC  
CGTGTAAATGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGCTAAAGCTAGGAACATCAGGTGCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACCTGGATAAGAAAATTGGCAGTTAGGCCCTTTCCCTTTCCACTA  
AATTCTTCTTAAATTACCATGTAACCAATTAACTCTCAGTGCACTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGGTAAAGGCCATATCCCCATG  
ATTATATAGTTATGCTACCTAATATGGGATATTCTGGGAATATGCCATTGCTAGTCAT  
TTTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCAGTCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGTACAGACATATACAGCATGTTACTG  
AATACGTAGGCAATAGTAACAGTGGTATTGTGATATGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATCTGTAACATGGTCACCTGTATAGGGCACTTACACCGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCCTAGGACATTA  
TTGAACACTGCCAGACGTTAAATACTGTATGCTTAAGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTTCTTAAATTAAACATAAGTGTACTGTAACATTACAAACGTTTAAATT  
TTAAACCTTTGGCTTTGTAAACACTAGCTAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSPGSEFWPYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPFLFEDESSSFHKRQFPVKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEELRQVGWSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPSTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCATCCGACTAGTTATTGAGCATCGCTCTCATATCACAGTGGCCATC  
TGAGGTGTTCCCTGGCTGAGGGTAGGCACGATGGCCAGGTGCTCAGCCTGGTGTG  
CTTCTCACTTCATCTGGACACAGGAGCTCTGGTCCAAGGCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGATCGAGAAATTATGGGATCACCCCTTGAGCAGAAAAGGCGAACCCAGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCTGTAGGCTGTGGACTAAGTTGGCCGGAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA  
TGGATTCTGGTCACTCTAGGATTAGCCAAACCCAAGGTGAGCTGGGAAAATGGGTGGGT  
TCCGTATTGGAAAGGTTCCAGTGAGCGACAGTTGAGCCTATTGTTACAACATCTGTAT  
ACTTGACTAACCTGTGATTCAGAAATTATCACACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACACAGAATTATTGTCACTGTGAGCTACCTACTCGGTGGCATCCCCCT  
ACTCTACAATACCTCTACTACTCTCCTGTCACTGTTCCACTTCACTTCAACGG  
AGAAAAAAATTGATTGTGTCAGAAAGATTTTATGGAAACTAGCACCATGTCAGAAC  
TGAACCATTTGTGAAAATAAAGCAGCATTAAGAATGAAGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGGTAGTGTCTCTCTCTTGTGCTGAGCTGGCTGGATTGTTGC  
TATGTCAAAGGTATGTGAGGCTTCCCTTACAAACAGAATCAGCAGAGGAATGAT  
CGAACCAAAGTGTAAAGGGAGAAGGCCAATGATAGCAACCTAATAGGAATCAAAGA  
AAACTGATAAAACCCAGAAAGTCCAAGAGTCCAAGCAAACACTACCGTGCATGCC  
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCTGCCAGCTGGGAAATCAAAGGCCAAAGAACAAAGAAGAAAGTCCAC  
GGTTCTAACTGGAATCAGCTCAGGACTGCATTGGACTATGGAGTGCAC  
AAAGAGATGC  
CCTCTCTTATGTAAACCTGTCTGGATCTATCTCTACCTCCAAGCTCCACGCC  
TTTCTGGCTCTGGTAGTGTCTAAATACCTCAGTGGAAAAGGGAGGAGTGGCAAAGTGC  
GGACCTTAAACATCTCATCAGTATCCAGTGGAAAAGGCCCTCTGGCTGAGGCTAGG  
TGGGTGAAAGGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCC  
CCTCTCTAGCTCTGAAAGAGAAACCGTATCCACCTGACATGTCCTCTGAGGCC  
AGAGCAAAGGAGATGGCAGAAAAGTTAGCCCTGAAAGGCATGGAGATTCT  
ACCTAATCTCTGAAAGCTAAATAAAGAAATAGAACAGCTGAGGATACGACAGTACACT  
GTCAGGGACTGAAACACAGACAGGCTAAAGTGTGTTCTGAAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGCTCTACCACTGCTGATATTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAAATTCTATT  
GTTACAGAAATGATTACTAAGGAAGATTCTCAGTAAATTGTTAAAAGTAATAAATTCA  
ACAAACATTGCTGAAGTACTATATGTCAGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCTAAACATTGCACTAGTAGAACGCTATCTGGGAAGCTATT  
GTTTGATATTCTAGCTTACTCTCAAACCTAATTCTATTCTGAGACTAATCTT  
ATTCACTTCTCTAATATGCCAACCATATAACCTTAAATTATTAAACATACCTAAGAAG  
TACATTGTTACCTCTATATACCAAGCACATTAAAAGTGCATTAAACATGTA  
GCCCTCTTTTCAACAGAAGGGACTGAGAGATGCAGAAATATTGTC  
AGCATTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKPVSRQF  
AAYCYNSSDTWTNSCIPETTTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGCTTGGCACCTCTAATTGCTCGTGATTCGGTCCCGCAGCTTCACGATGG  
CTCGCCCCAACCTTACTACCTTCTGTCGCCCTGCTCTGCTGCCCTACTCGTAGGAA  
ACTGCGGCCGCTCTGCCACGGTCTGCCAACCGAAGACGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCTGATGTTCTCAGTGCCTATTGTGATGATGAAGAACCGAGA  
TCCATCACTGTGGAGAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTCCGCTTGGATATTGCACTGGCCTACTTACATCACACTGCACTGTTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGGAGTTCTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTGGAGGTGGATGTTGGACGCTATACTGATGTTAGTACCGGGTAC  
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCTGTTCCAAGGGCAA  
GGAGGCAATGGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCATGGACCTTCTG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATAACCAGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGGCTGTCATGGCTCAACCCCCACACAGTGTAGA  
TGGGGAAAACAAGAAGGATAAATAGATCTCACTTTGGCAGTGTCTCTCTGTCAAATT  
CCAGGCTTTCCATAACACAAAGCCTGAGGCTGCGACCTTNTATTNATGTTCCCTTGG  
CTGNGACTGGNTGGGGCAGCATGCGAGCTCTGATTTAAAGAGGCATCTAGGGAAATGTCAG  
GCACCCCTACAGGAAGGCTGCCATGCTGGCCAAGTGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGAAATGGTTCTCCAAGCTGGCTAGTGTGTTAACTGCTTATC  
AGCTTACAGACATCTCCATGGTTCTCCATGAAACTCTGTTGTTCATCTCCCTCTTAG  
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCACCCAAAGGACTCTGCTTCCCTAACGCCCTCTGGCTTATGGTC  
TTCATTAAAGTATAAGCTAACCTTGTGCTAGTCCTAACGGAGAACCTTAAACCAAAAG  
TTTTTATCATTGAGACAAATTGAAACAACCCCCCTATTGTGGGATTGAGAAGGGTGAA  
TAGAGGCTTGAGACTTCTCTTGTGTGTTAGGACTTGGAGGAGAAATCCCTGGACTTCA  
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCTGTAATAAAAAGATTGGATT  
TCCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFMSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGGGCCCCCGAGAGCTAGCCGTGAGGAAGCTGGCTGGGACGTTGCCCTG  
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGCCTGCTCCCTGGTCCA  
TTGCTCTGCTGCCGGCTCTACGGACTGCCCTCTACAAACGGCTCTACTACTCCAACAG  
CGCCAACGACCAAGAACCTAGGCAACGGTATGGCAAAGACCTCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCTGTTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCTGGTCTCCCGCGCGTGTGCGTGTCAAATGGTGAAGCT  
GTCGGAGAACGGGGCCCGAGAGAAGGACGTGCTGGTGGCATCGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGCTGGAGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGGTCTTCCCTACAGTCCCCA  
ACGGGCCTACCACTTCAACTTCCAGGGCCACAGGTCTGTGAGACAGGCTGGTG  
GTGGCCTCTTGGAGCAGCTTCCGGCCTGGAGGAGGGCTGGACTGGTGCAACCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGGTGCACGGCCACCCCTGCGTGGCC  
CAGGGCTGGCACCTGGCGTGCAGAGCTACGGCCCCGCCACGCCGCCTGCACCGTATGAT  
GTATTCTGCTTGCCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAACGCT  
GACGCTGACAGAGGCAAGGGGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTTGGAC  
AGCTTTGCCCTGGAGTCCATGGCTGGACCGCTGCGACGCTGGCTGGCTGGAGAT  
GGCAGCGTCCCGTACCCCTGTGGTCACCCGATCTAACGTGGGCCCCAGAGCCTGGGT  
CCGAAGCTTGGCTCCCCGACCCGAGGGCGCTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGGCCCTCCCTGCCGATCCCTCACTGGCTGTGTATTATTGAGTGGTT  
CGTTTCCCTGTGGGGTGGAGCCATTAACTGTTTATACCTCTCAATTAAATTCT  
TTAACATTTTTACTATTTTGTAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCTG  
GATGCCCACTCCAGGAATCATGCTGGCTCCCTGGGCCATTGGGGTTTGTGGCTCTG  
GAGGGTCCCCCAGGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGCAGACTGGC  
GGTGGCCTGCTAGAATGCCCGGGAGTCGGGAGTGGGGCACAGTCTCCCTGCCCT  
CAGCTGGGGAAAAGAAGAGGCCCTGGGGCTCCGGAGCTGGGCTTGGGCTCTCTG  
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCAGGAAATCTGAGGGAGGAAGAAACTCCCCCCCCGTCC  
TCCCTCTCGGTTCAAAGAATCTGTTGTGCTATTGTTCTCCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGACTTTGACAATAATGGTGTATGACTGCCCTCCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLLEDYGRYCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEGLDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRLRHRYDVFCFATALKGRRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**GAT**GATGTGGCACCACATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCAGACGCCAGGCCCCATGGC  
CAGGGGAGGGTGCACCAGGCCCGCCCTGAGCGACGCTCCCATGATGACGCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGGCGATCGGACCGCATGGACGCCGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGATCGGCACACGCAGCGGCA  
CATACGGGACTCGGTGAGCGGGCCTGGGACACGTACGACACGGACCGCAGGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGGGCACTACCGCCCGGTGAAGAATTCTATGAC  
GTGGAGGATGCAAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGCGTTTCCGGTGGC  
CGACCCAGGATGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCACCCCGAGG  
AGTTCCCTCACATGGGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCTGGGTGACACGGAGGGCAGCAGTCCGGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGGCACTGGGTGCTGCCCTGCCAGGACGCC  
CTGGTGGAAAGCCAACCACTGCTGCACGAGAGCGACACGGACAAGGATGGCGCTGAGCAA  
ACCGGAAATCTGGTAATTGGAACATGTTGTGGGCACTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCACGATGAGCTG**TGAG**CACCGCAGCCTGCCACAGCCTCAGAGCCCG  
ACAATGACCGGAGGAGGGGGCCGTGTTCTGGCCCTCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGGCTCTCAGGGACCCCTGGGTGGCTTC  
TGTCCCTGTCAACCCCCAACCCCGAGGGAGGGGCTGTCTAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGGCCAGACCCAGGGACCTTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCAACCCCTCCAGCTCCAAATCTGAGCCTCACCACATAGACTGAAACTCCCT  
GGCCCCAGCCCTCTCCGTGGCTGGCCTGGGACACCTCCTCTGCCAGGAGGCAATAA  
AAGCCAGCGCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDRDGRVGWEELRNATYGHYAPGEEFHVEDAETYKKMLARDERRFRVADQDGDSMATE  
ELTAFLHPEEFFPHMRDIVAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

# FIGURE 81

GGGGCCTTGCCTTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGGAGCCCCGG  
GGGGCGGGCGGGGTGCGAGGGATCCCTGAGCCTCTGTCCTGTTCTTGCGCTCCAG  
CCTGTCCTGTCGTTTGGCGCCCCGCCCTCCCGCTGGGGGTTGCAACCGATCTG  
GGCTTCGCTGCAATTGGCGCAGGCGCTCCAGACACTAGAGGGGCGCTGGCTGGAGCAG  
CGGGTCTGTCGTTCTCTCTCTGCGCAGGGAGCTCCAGACACTAGAGGGGCGCTGGCTGG  
GAGGAGGTGACCGCGGGGCCCTCCGCACCCCTGGCTTGGCCGATTCTCCCTCTCCAG  
GTGTGAGCAGCTATCAGTCACCATGTCCCGAGCCTGGATCCCGCTCTCGGCCCTGGTGTG  
TGTCCTGCTGCTGCGCCGGGGCCGGAGCAGGAGGGAGCCGCTCCATTGCTATCACATG  
TTTACAGAGGCTTGGACATCAGGAAAGAGAAGAGCATGTCCTGCCCAGGGGGCTGCC  
CTCTTGAAGGAATTCTCTGTTGATGGAAACATAGTATGCTCTGTTGAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACTGTACGAGTCTATAGCTACC  
TGTCGAGAAAACATTCTCAGTAGATGCCAACATCCAGCTCAAAATGCTTCTAGAT  
GGTCTGCTTCTTACAGTAATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAAGACTAAAGAAAACACCCGAGAAGAAAAGTGG  
CAATAAAAGATTGAAAGCAGACATTGCTATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTAAATTACAGAAAGATTGTTGAAAAGTGGCTTAATGTTGGAATTGGAACA  
GAAGGACCCATGTTGGCCTTCTCAAGCCAGTAACATCCAAATAGAATTAACTGAA  
AAACTTACATCAGCAAAGATTTGTTGCTTAAGGAAAGTAGGTTAGGGGTAA  
ATTCACATACAGGAAAGCCTGAGCATACTGCTCAGAAATTCTCAGGGTAGATGCTGG  
GTAAGAAAAGGGATCCCAAAGTGGTGGTGTATTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGATTGTTGGCAGAGAGTTGGTGTCAATGTTATAGTTCTGGCCA  
AGCCTATCCCTGAAGAACCTGGGATGGTCAAGGATGTCAATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTCTTACATGCCAACATGGGCAACTGGTTGGCACCAAAATACGTAAA  
GCCTCTGTCAGAACAGCTGCACTCATGAAACAAATGATGTCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCCTC  
ATGCTGAAATTGTTGAAACATGCAAGACTTTGAGATCTGGACATTGGTGCAGAAGAT  
AGCTGCTGACAGTTACTTATGATCAGGCCAGGGATTCTAGTTACTGACTATAGCACC  
AAAGAGAATGTCAGCTGTCACTAGAAACATCCGCTATATGAGTGGGAACAGCTACTGGT  
GATGCCATTCTCTTCACTGTTAGAAAATGTTGGCCCTTAAGGGAGAGGCCAAACAGAA  
CTTCCCTAGTAATTGTCAGATGGCAGTCTTATGATGATGTCAGGGCCCTGCACTGCTG  
CACATGATGCAAGGAAACTACTATCTTCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAAAGAGGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCAGAGGCAATTGAGAGATTCTTAAATCCAGCAAT  
AATGGTAACATTGTCAGAGGCAACTGAGGAAAGTACAAGGGATCCAGTGTGAAATTGATT  
CTCATAATACTGAAATGCTTAGCATACTAGAATCAGATAACAAACTATTAAGTATGCAAC  
AGCCATTAGGCAATAAGCACTCCCTTAAGCCGCTGCCTCTGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCAATCATGGCTTCTAGAAAACCTCAGGAAAGAGGA  
GATAATGTCAGGATTAACCTTAAGAGTTCAACCAGCTACTAAATGTCAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACCTAGACCAAAAAAA

## **FIGURE 82**

MSAAWIPALGLVCLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSTSQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQQRRFNLQKN  
FVGKVALMLGIGTEGPHVGVLVQASEHPKIEFYLNKNTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNAIFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLA  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYYDDVQGPAAAHDAGITI  
FSGVVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGCACCGGGGCCACCGGCCGCTCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCGGGGAGCGAGCAGATCCAGTCAGGCCCGCAGCGCACTCGTCCAGTC  
GGCGCGGGCTCGGGCGCAGAGCGAGATGCAGCGCTGGGCCACCTCTGTGCCCTGC  
TGCTGGCGCGCGTCCCCAACGGCCCCGCGCCGCTCCGACGGCACCTCGCTCAGTC  
AAGCCCGGGCCCGCTCTAGCTACCGAGGGGCCACCCCTCAATGAGATGTTCCCGA  
GGTTGAGGAAGCTGATGGAGGACACCGCAGCACAAATTGCGCAGGCCGGTGGAAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT  
CACATGAGAACACACAGAACAGAAGGTTGAAATAATACCATCCATGTCACCGAGAAAT  
TCACAAGATAACCAACACAGAACAGACTGGACAAATGAGTCTTCAAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAGGCGAGAAGGAGGCCACGGTGCATCATCGACGGACTGTGGGCCAGC  
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGGCATGCCGGGAGGATGCT  
CTGCACCGGGAGCAGTGAAGTCTGAGGACAGCAGCTGTGTCAGTGCACCCAAA  
TGGCACCCAGGGGAGCAATGGGACCATCTGTGACAAACAGAGGACTGCCAGCGGGCTG  
TGCTGTGCCCTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA  
GCTTTGGCATGACCCGCCAGCGCCCTTGAGGACTCATCACCTGGAGCTAGAGCTGTG  
GAGGCTTGGACCATGCCCCCTGAGGAGGAGCTGGCAGGAGCTGGCAGGAGCTGG  
GTGTTATGTGCAAGCGCAGCTCTGTGGGAGCGTGACAGATGGGAGATCTGTG  
CAGAGAGGTCCCCGATGAGTATGAAGATTGGCAGCTTCATGGAGGAGGTGGCAGGAGCTGG  
AGGACCTGGAGAGGAGGCTGACTGAAGAGATGGGGAGGAGCTGGCCTGCCCGCT  
GCACACTGTTGGGGAGAGAGATGAGATCTGGACAGGCTGTGGTAGATGTGCAATGAA  
ATAGCTAATTATTCAGGTGTGCTTAGGCGTGGCTGACCAGGTTCTCTCTACA  
TCCTCTCCAGTAAGTTCCCTCTGGCTTGACAGCATGGGTGTTGTGATTGTTCTGAGC  
TCCCCCAGGCTGTTCCAGGCTTCAGCTGTGCTGGGAGAGTCAAGGAGGTTAAAC  
TGCAGGAGCAGTTGCTGCCACCCCTGTCAGATTATTGGCTGTTGCTTGCCTACCACTGGCAG  
ACAGCGTTGTTGTTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACATCAA  
AGTCTCCCTCTGATTGGTTTGGGAAATCTGGAGAGAGATGGCTTGGCAAAACATCAA  
CTGGCAAAATGCAACAAATGAAATTTCACAGCAGTTCTCATGGCATAGGTAGCTG  
TGCCCTCAGCTGTTGCAAGATAATGTTCTGTCACCCCTGCAATTACATGTTTATTGATCC  
AGCAGTGTGCTCAGCTCTACCTCTGTGCTGGCAGGAGCATTTTCTATCAAGATCAATTG  
CCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCTGTGCTTGGCAGGAGATCTCAGAG  
GCTCAGAGACTCAAGCTGCTGCCCAGTCACACAGCTAGTGAAGACCAAGAGCAGTTCT  
CTGGTTGTGACTCTAAGCTCAAGTGTCTCTCCACTACCCACACCAGCCTTGGTGCACCAA  
AACTGCTCCCCAAAAGGAAGGAGAATGGGATTITCTGAGGAGCATGCACATCTGGAATTAAAG  
GTCAAACTAATTCTCACATCCCTCTAAAGTAAACTGTTAGGAAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCGCTCTCTAATGAGAACATGATATTGACACTGTCCTCTTGGCAGT  
TGCAATTGAGTAATTGAGGGCAGGATTATAATGAAATTTGCAAAATCACTTAGCAGAAC  
GTACTATTAGGTAATTGAGGGCAGGATTATAATGAAATTTGCAAAATCACTTAGCAGAAC  
TGAAGACAATTATCAACCAACGGAGAAAATCAACCGAGCAGGGCTGTGAAACATGTT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGAAGTGTGCAACCATGTTACATCCAGAGTTCTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGATAAAACATAACTGTCATTTAGAAATCAAGC  
ATAAACTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRIGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEEMEAEEAAAKASSEEVNLPPSYHNETNTDTKVGNNNTIHVHREIHKITNNQTG  
QMVFSETVITSGDDEGRRSHCI IDEDCGSPMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQGLCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVDEYEV  
GSFMEEVVRQELEDLERSLTEEMALGEAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

# **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHPVCPQQCACQIRPWYTPRSSYREATTVDCNDFLTA  
VPPALPAGTQTLLQSNSIVRVDQSELGYLNLTTELDSQNSFSARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQEYLNLHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRRPLANLRSVLVLAGMNIREISDYALEGLQSLSESLSFYDNQ  
LARVPVRALEQVPGKLFDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHLPQMELTMNNNNALSAHQQTVESLPNLQEVEGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPPEPEIYWVTPAGLRLTPAHGRYYRVVPEGTLELRRVTAAEEAGLYT  
CVAQNVLVGADTTKTVSVVVGRALLQPGRDEGGGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLILLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV  
SAPLVLWPWNPGRKLPRLPRSEGETLPPQLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

## **FIGURE 88**

MRQTI I KVIK FILI ICYT VYYVHN IKFDV DCTVD I ESLT GYRT YRCAHPLATLFK ILASFYI  
SLV IFYGLIC MYTLWWMLRRS LKKY SFESI REESSY SDIPDV KNDFA FMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQNLNNNEW TLDKLRLQRLLTKNAQDKL ELHLFMLSGIPD TVF DLV LEV  
LKLELIPDVTI PPSIAQLTGLKELWLYHTAAKIEAPALAFLREN LRALHI KFTDIKEIPLWI  
YSLKTLEELHLTGNL SAENNR YIVIDGLRELK RLKV RLKS NLKLPQVVTDVGVHLQKLSI  
NNEG TKLIVLNSLKKM ANLTEL E LIRCDLERI PHSIFS LHN LQEI DLKD NN LKTIEE IISFQ  
HHLRLTCLKLWYNHIA YIPI QIGNL TNLERLYL NRNKIE KIPT QLFYCRKLRYLDL SHNN LT  
FLPADIGL LQNLQNLAITANRIETLPP ELFQ CRKL RALH LGNN VLQSLPS RVGE LTNL TQIE  
LRGNRLE CLP VELGEC PLLKRS GLV VEEDL FNTL PPEV KERL WRA DKBEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTTATTATGCCACCAACTCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGGCGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCTTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGGTTCTCTGAAGACCTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTCCATTCTACATTTCCTCAGAGTCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTACAGCAGGGACCATCAAGTCAACATTGCGGGGT  
TGCCCTGGGTGATTCTGGATCTCCCTGTGATTGGTCTCTCTGGGACCTTAACCTGT  
ACAGCATGTCCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGGTGCAGAGCAAGTA  
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACATAAAAGCCTCCCA  
CGTCTACAATGGAGTCAGACTAGAATTCAACAGAGCCACCTAGTTGTCTTGTCAAGCGC  
CACGTGAGACACCTACAAACAGAGATGCCCTAACGCCAGTCATGAATGCCCATCAGAAAGAA  
GCTCAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACAAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTGTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGTCAGGAGGCCCTG  
GGTGGGAAACTGAAGTGGCAGAACTGCCCTAAATTCACTGAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGCACCTAAATCTTGGAAACATCTGCTTGTCAAGTCCTACAAAGAACCTTGTCTTC  
TACTGGATTCTGAAAGCTGGTCAATGGTCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTIONCAAGAAATGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCT  
AACTGGGCTGTGATCAAGAAGTTCTGACCAAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCTGCTCTAAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTFGSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVSVLSPWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGGLYRE  
ATELGWGKAEMIIEQNTDGVNFYNIITKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQDL  
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKMLAFYWILKAGHMVP  
SDQGDMALKMMLRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGGGCC**T**GGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTACAGGACCATGCGGCCGA  
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCAACTCGGCCTGGCCGTGGCA  
GGGGAGCCTGCCGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG  
CACTCACGGCGGCCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCACTAACACCG  
TTACTTCGTATCGAATATCTATCTGAGCCTCGCTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGTGCACTGTGACCTACACTAAACACATCAGGCCATCTGCTCCAG  
GCCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCACACCCCTCCAGGAAGTTCAGGTGCCATATAACA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCCAAGGACATCTTGAGACATG  
GTTTGTGCTGCCAACGCCAACGGGGAGGATGCCCTGCTTCGGTGACTCAGGTGGACCCCTT  
GCCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCCGGTCTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG  
CTGATGGCCAAGAGTGGCATGTCAGGCCAGACCCCTCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCT**G**AGCCTACCTGAGCCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTCTTCTGCTTGTTGGTAAAAACACATTCCAGTTGA  
TGCCCTTGAGGGCATTCTCAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLRARAGLRKPEAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW  
DSHVCGVSSLSHRWALAAHFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDGGPLACNKNG  
LWYQIGVVSVWGVGCGRPNRPGVYTNISHHEWIQKLMAQSGMSQPDPSPWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCCCACGCGTCCGGCAGCGTGGGAAGGGCAGA**ATGG**GACTCCAAGGCTGCCCTAGGGCT  
CTTGGCCCTCATCTCTCTGGAAAT**CAGT**TACGCCGGAGGCCGACCAGCGGAGGGACGC  
TGCCCCCGAGGGTCTCCCTGGGGCGGTGCGGACCTTGAGGAAGAGCTGAGTCACCTT  
GCCCTGAGACAGCAGAAAT**TG**GGAAAAGACTCTCGGAGCTGGTCAGGCTGTGCGATCCCAG  
CTCTCTCATACAGGGAAATACCTGACCCATTAGAGAAT**TG**GGCTGATCTGGTAGGGCATCCC  
CACTGACCCCTCACAGCGTCAAAAT**TG**CTTGGCAGCGGAGGCCAGAACAGTGGCATTCT  
TGATGACACAGGACTTCTGACTTGTGCTGAGCATCCGAAAGCAGAGCTGCTGCTC  
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGAAACCCATGTGTAAGGTC  
ATCCCCATCCACAGCTTCCACAGGCTTGGCCCCCATGGACTTGTGGGGGACTGACCGT  
TTCCCCCAACATCATCTGGAGGCAACGTCCTGAGCGCAGGTGAGCAGGGACTGTAGGCT  
GCATCTGGGGGATAACCCCTCTGTGATCTGAAAGCATACAATTGACCTCAACAGAGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCTGTGCCAGTTCTGGAGCAGTATTTCCATGAC  
TCAGACCTGCTGCTGAGCTTCATGCGCCTCTGGTGGCAACTTGTGACATCAGGCGATCAGTG  
CCGTGTTGGTGGACAACAGGGGGGGGGGGGGGGGGGGATTGGCCAGTCTAGATGTCAGT  
ACCTGATGAGTGTGCTGGTGGCAACATCTCACCTGGGCTACAGTAGGCCCTGGCGGAG  
GGACAGGAGGCCCTCTGTGAGTGGCTACGTGCTAGTAATGAGTCAGCCCTGCCACATGT  
GCATCATGTGAGCTATGGAGATGATGGAGACTCTCTGAGCAGGCCATACATCCGGGGTC  
ACACTGAGCTCATGAGGCTGCGCCTGGGGTCTCACCTGCTCTGGCCTCAGGTGAGCATG  
GGGGCCGGGTGGTGGTCTGTCTCTGGAGACACCGAGTCCGCCCTACCTTCTGGCTCCAG  
CCCCATGTCACCAACAGTGGGAGGACATCTCTCAGGAACCTTCTCATTCAACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTCAGGAATGTCTTCCACGGCCATCAGGAG  
GAAGCTGTAACGAAGTCTCTGAGCTCATGGCCCCACCTGCCACATCAGGTTACTCAATGC  
CAGTGGCGTGCCTACCCAGATGTGGCTGACTTCTGATGGCTACTGGGTGGTCA  
GAAGTGGCCCATTCCTAGGGTGTGGCAACTCTGGCCTCTACTCCAGTGTGGGGGAGTC  
TCTCTGTGATCAATGAGCACAGGATCTCTAGTGGCCGGGGCTCTGGCTCTTCATCA  
GCTCTACCAAGCAGCATGGGGCAGGTCTTGTGTAACCCGGTGGCTGCCATGAGTCTGTC  
TGGGATGAAGAGGTAGAGGGCCAGGGTGTGGCTCTGGTCTGGTGGGATCTGTAACAGGC  
TGGGGACACCAACTTCCCAGCTTGT**GA**AGACTCTACTAACCCCTGACCCCTTCTATC  
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTCTCAGTCCCTTATCTGCCCTGTG  
GAAGGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAAGACAGCTTATCTCTAACCCCTGAAA  
TGCTGTGAGCTTGTGACTCTGCCAACCTTACCATGCTCCATCATACTCAGGCTCTCTACT  
CTCTGGCTTAGAATCTCTCAAAAGGTTGATACAGTATTGTGATGCTCTCCCTCCG  
ATCTCATTTCTTCACTCAGGTTTCTCAAAAGGGTTGATACAGACTCTGTGCACTA  
TTCACTGTGATATTCACTTCCCCTCAACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TCTCTACCCCTGACATCCAGAAACATGGCCCTCAGTGCTACATCTCTCACTTGTGTTTATG  
GCCCTTCTCATCATAGTGGCCACTCTCTCTACTTACTGCTTCTCAGGCTTCAACTCTCTG  
ACTACTCTGTCTTCTCTCATCAATTCTGCTCTCATGGAATGCTGACCTTCAATTG  
TCCATTGAGATTGCTCTCTCAGTTACTCATTGCTCCCTGAAACAAATCACTGACA  
TCTACACCAATTACCATCTCACTAAAGACTTCTATCCAATAATGATTGATACCTCAA  
TGAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPYQGKYLTLENVADLVRPSPLTLHVTQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLQRQP  
EPQVTGTVGLHLGVTPS VIRKRYNLTSDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDDESLSSAYIQRVNTELMKAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGSNSVFPRTSYQEEAVTKFLSSSP  
HLPSSYFNASGRAYPDVAALSDGYWVVSNRVIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDVEVEGQGFCSGPWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

## **FIGURE 96**

MAGIPGLLFLLFFLCAVGQVSPYSAPWKPTWPAYRLPVLPQSTLNIAKPDFGAEAKLEVS  
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSGKSR  
RRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKLRVGFLPKFKDGGRGANDSTSAMPEQMFKQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKPKPHRKFKMKGVSPPAKQLPGGRIHFGSYDNDRPGNLVYRFCDVKDETYDLYQQCD  
AQPGASGSGGVYVRMWKRQQQKWERKIIIGIFSGHQVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATCGCCCTGGGTCCTCGAGCTGCTGCCGTCCCCCGCCCCACAGCC~~ATGGTGGTT~~  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCGGCACCTCACCTCCCTGCTGCTGCTG  
GCCTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCCAGCCTGTTGGGAAGCCCCA  
GCAGCTAACCGGGTTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAGAAATGGGACCCACACTGCGCAGGTTCTGCTCACAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCTGGCTCTCGTCTCCAGAAGGTGGGTGTTGCTGGGTGGAGC  
CCCACCCCTGTATTCTTGGAAAGGAAGGTGCTGTGAGACATTGCCCTGGTGCGTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCATCTGCCCTACCTGATGCCCTATCCACCT  
CCCTCCAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC  
CCCACCCCTCAGACCCCTGAGAAGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT  
CTGTAAGTGGGGAGCAGGGACAGGACAGGGACCCATCACTGAGGACATGCTGTGCTGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCAGCTCGGGGCCCTCATGTCGCCAGGGACG  
GCGCTGGCTGCTGGCGCATCATCAGCTGGGGAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCTGGTGAGAAGATCGTGAAGGGTGCA  
GCTCCGCGGGCGCCTCAGGGGGTGGGCCCTCAGGGCACCGCAGGGCTCTGGGGCG  
CCGCGCCTCT~~AGGGCGCAGCGGGACCGCGGGCTCGGATCTGAAAGGGCGCCAGATCCACA~~  
TCTGGATCTGGATCTGCGCGGGCTCGGGGGTTCCCCCGCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGAGGGCTGCTGGAAAGGAAACCCCCCTCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCTGGCC  
GACTTCCGGCCCCGCCGGGGCCCCAGCGCTTTGTGTTATAAAATGTTAATGATTTTAT  
AGGTATTGTAACCCCTGCCACATATCTTATTCTCCAATTCAATAAATTATTATT  
CTCCAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAAIPVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWTITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRQKVGA  
WVEPHPVYSWKEGACADIALVRRLERSIQFSSERVLPICLDPASIHLPPTNHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLDGSGGPLMC  
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCACTGCTA  
CTGCTGGTGGCCACCAAGGGCCGTTGGACCCCTCACAGATGAGGAGAAAGTTGATGGT  
GGAGCTGCACAACTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGTCACATGA  
GATGGGACGAGGAGCTGGCCCTCGCAAGGCCTACGCACGGCAGTGCCTGCCCCAC  
AACAGGAGCGGGCGCCGCGCGAGAACTCTGTCGCATCACAGACGAGGGCATGGACGT  
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAACACTAACACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAGCTCAGGGTGTGGAGGAGCAACATGAATTACT  
GGTGTGCAACTATGAGCCTCGGGGAAACGTGAAGGGAAACGGCCCTACCAAGGAGGGACTC  
CGTGCTCCAAATGTCCTCTGGCTACCAACTGCAAGAACTCCCTCTGTGAACCCATCGAAGC  
CCCGAAGATGCTCAGGATTTGCTTACCTGTAAC TGAGGCCCCATCCTTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCGCTGTGGAAACCCAGGCC  
CCAACCTCCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTTGCCTAAC  
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTCTGGATGAGGAGGCCAGTTA  
CCTTCCCAAATGACCCATGTCCTATCCAAAATCAGCAGACAAAGTGAACAGACAAAACA  
AAAGTGCCTCTAGGAGGCCAGAGAACTCTGACCCAAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCATGCCAGGAGGAGGTGAGGCTGAGTTGCCTCCCTCAGTG  
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCTCCAGTCCCTGCCAATTCCCAAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCGCAGTCGTCCTGGCAGGTGCAAGGGCCCTGACA  
AGCCTAGCGTTGTCAGGGCTGAACCTGGCCCTGGCATGTGTGGGCCCTCTCTGGGA  
CTACTGCTCCTGCCCTCTGGTGTGGCTGAATCTCTGAATGGGATACCACTCAAGGG  
TGAAGAGGTCACTGTCCTCTGTCACTTCCCCACCTGTCCTCCAGCCCTAAACAAAGATA  
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCCACAGGCCCTGGCTGGCTGGAGCTCAGGAGGCCCTGAGGACTGCCACCC  
GGGCCACACCTCTCCTGCCCTCCCTGGTGAAGTCCCTGGGGTGGAGGAGTTGAGGGAGCT  
CACTGCCTACCTGGCTGGGCTGTGCCACACGACATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTT  
TTTGAATGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCAATAAAACCT  
GTCCAACCTGTGAAA

# **FIGURE 100**

MHGSCSFLMLLLPLLLLWATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCWGHNKERGRGENLFAITDEGMVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCTVTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAEAEAEELPPSSEVLAS  
VFPAQDKPGEQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNNSGPGBHVWGPLLGLLLLPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

**FIGURE 101**

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETPNLGPV SAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELTQAFPALQLKYLYLNSRNRTSMEP  
GYFDNLANTLVLKLNRRNRIASIAPPKMFKLPQLQHLELRNRIKVNVDGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGSLSNMEILQLDHNNLTEITKGWLWGLMLQELHLSQNAINRISPDAWE  
FCQKLSELDLTFNHLSSLRDLDDSSFLGLSLNNTLHIGNNRVSYIADCAFGRGLSSLKTLDDLKNNE  
ISWTIEDMNGAFSGLDKLRLRLLQCNRIRSITKKAFTGIDALEHLDLSDNAIMSLQGNNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLQPQWVAENNPFQSFVNACAHPLQLLKGRSIFAVSPDGVC  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG  
GEVMEYTTILRLRREVEFASBEGKYQCVCISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPPAQIAWKDGGTDFPAARERRMHVMPEDDVVFI DVVKIEDIVGVYCTAQN  
SAGSIISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAAGGSPPPKNWTKDDSPLVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCMNSLTGTERGNRLSVIPTPTCDSPQMFTAPSPLDDDG  
WATVGVVIIAVVCVVGTSLSVWVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLLAD  
RQDGYVSSESMSGHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDFETYHTGCSFDPTRTVLMHDYEP SYI KKECYPCHPSSEESCRSF SNISW  
PSHV RKLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDQEENHICFKQTLENYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGCTTGCGTGCACAAAGTGA  
AAGGATGCAAGGACGCCGCTTCCTCCTGAAACGCCAATGATAACTGATTTGCAAGAGAGAAGAAC  
GAAGCTTTTCTTGAGGCCCTGAGCTTAAACAAATGTGTATATGTCACACAGGGAGCATTAAGAATGAAA  
TAAACCCAGAGTAGACCCGGGGGGTGGTGTGCTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCTCC  
CCACCCCCAAAAAAAGGGATGATTGAAATGAAAGAACGGAGGATTCAAAAGAAAAAGTAGTGTCTATTCTC  
TATAAAGGAGAAAGTGGAGGCCAAGGGAGATAATTGGATGAAAAGTGGGCTTTTTAGTAAAGTAAGAACT  
GGTGTGGTGTGTTTCTCTTGTGAATTCCAAAGAGGAGGAAATTAAATAATACATCTGCAAAGAAA  
TTTCAGAGAAAGAAAAGTGTGAGGCCGGCAGATTGAGCTGGGAGAGAAAACAGCAGACAGCTTGG  
TTTGCCCTATGTGACTAAATTGAGCAGATAATTGAGCTGGGTTTCTCATCACCTCCCTTTTTAAAT  
TTTATTCTTCTTGGTATCAAGATCATCGCTTCTCTGTTCTAACACCCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAACTAACACTTGTGAATTCCAGAAAGGCCAACACAGGATAAAATTATGATGTGAA  
GACCTTACATCCACAGCAGATAATGAGTTCACTAGGGCTTAAACAGGGCTTATTGACCCCTGCTTGGTGT  
GCTGGCTCTTACCTCTGTGTGGCTGGTCTGGTCTGGGCTCAGACCTGCCCTCTGTGCTCCCTGAGCAA  
CCAGTCAAGGCTGATTGTTGCTGGGAAACCTGGCTGGAGGATGGGATCTCCACCCACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCAGATCATCAAAGTGAACAGCTTCAAGCACTGAGGACTTGGAAATCT  
ACAGTTGAGTAGGAACTTCAAGAACATTGAGAAATTGGGGCTTCTGGGAAACCTTAAACACTCTGGA  
ACTCTTACATCTCTTACTACATCCGGAAATGGGCTTCTGGTCTTAAAGAATTCTTCTGGGAACT  
GGGAACAAACCCCTGAGAACGCTCCCTTAAAGAATTCTTCTGGGAACTTGGGCTTCTGGGAAATCA  
CATGTGCAACCTCTGGGAATCTTCAACCTCACACCGCTCATAAAACATGAGCTGGATCTTCTGGGAAATCA  
TTTATCTGCATCAGGCTCTGGCTTCAACCTTCAAGGTTTGTGACCTTCAAAACTGTGAGTATGAGCTTGG  
TCAAGTATTGAAACGGATGCTTCAACCTTCACTGACTTGTGAGTATGAGCTTGGGACACAATAATCTAAC  
ATTACTGCTCATGACCTTCTACCTCCCTGATCATCTAGAGGGGATACATTAACTCACAACCCCTTGGGAAC  
TAACTGTGACATACTGGCTCAGCTGGTGGAAAGATAAAAGACATGGCCCTCTGAAACACAGCTTGTGCT  
TAACACTCTCCAACTTAAAGGGAGGGTACATTGGAGAGCTGGACCCAGAAATTACTCACATGCTATCTGG  
GATTGTGGAGCCCCCTGAGACCTCAATGCACTGAAGGACATGCACTGAGCTGGGACCCAGCA  
CTTGACATCTGATCTGGAAATTACTCAAAATGGAAACGCTCATGACACATGGGGCTACAAAGTGGGATCT  
GCTCAGTGTGATGGTACGTTAAATTCAACAAATGTAACTGTGCAAGATACAGGGCATGTACACATGTATGGT  
TTCCGGTGGAAATACTCTGCTTCAACCCCTGATATTGTTACTCTGACCAACACTTCTTCTCTTACTTT  
AACCGTCACACTAGAGACTTGTGAAACCGTCTCAGGATGAGGGCAGGACACAGATAAAATGTGGTCCACTCC  
AGTGTGCACTGGGAGACCCAAATGTGACCCCTCTCACAACAGAGGACACAAGGTTGACAGAGAAAACCTT  
CACCATCTCCACTGACTGATATAAACAGTGGGATCCAGGAAATTGAGAGGTATGAGAAGTACACAAATCTCAT  
TGGGTGTTTGTGGCATCACACTCATGGCTGGCAGTGATGCTGTCATTCTACAGATGAGGAACCCAG  
TCGGAAAACCATGACCCCAACAGGACTCTGGAAATTATTAAATGTGGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCCATGCTCTGATCAGGATGAGGCCCTAAATCACTATACTCATACAAATCTCCCT  
CAACACACACACAGTTAACACAAATCTCAATACAGCTCAGTGTGAGTGAACCGTTATTGATCGGAATGAA  
CTCTAAAGAACATGTACAAGAGACTCAATCTAAACACTTACAGAGTTACAAAAAAACAAAACATCAAAAAAA  
GACAGTTTAAAGAACATGACCAAATGACTGGGCTAAATCTACTGTGTTAAAAAAAGTGTCTTACACAAAAACAA  
AAAAAGAAAAAAATTATTATTAAACAAATTCTATTGTGATCTAAACGACACAAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSCSNCFSKVIC  
VRKNLREVPDGISTNTRLNLHENQIQIIVNSFKHLRLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKEWLWRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLMCNLREIPNLTPLIKLDEELDSGNHLSAIRPGSFQGLMHQKL  
WMIQSQIQVIERNNAFDNLQSLVEINLAHNLLTLPHDLFPLHHLERIHLHHNPWNCDIL  
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYYFTCYAPVIVEPPADLNVTGMAAE  
LKCRASTSLTSVSWITPNGTVMTGAYKVRIAVALSDGTLNFTNVTVQDTGMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTDDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

## **FIGURE 106**

MSAPSILRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSIKASMSHLQSLREVKLNNNELETIPNLGPVANSIT  
LLSLAGNRIVELPEHLKEFQSLETLDLSSNNISELQTAFFALQLKLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRIISAIPPKMFKLQLQHLELNRNKIKNVGDLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSLNMEILQQLDHNNLTERITKGWLGYGLLMLQELHLSQNAINRISPDAEFC  
QKLSELDLTFNHLSRLDDSSFLGLSLLNLTIHGNRNSVYIADCAFTRGLSSLKTLSDLKNNEIS  
WTIEDMNGAFSGLDKLRRLLIQGNRIRSITKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLLHNTSSLLCDCQLKWLQPQWVAENNFSQSFVNACAHPPQLLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNEHHDAEMENYAHLRAGGE  
VMEYTTILRLREVEFASEGYQCVSNHFQSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAVGHPAPQIAWQKDGTDFPAAERRMHVPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSSPPKLNWTKDDSPFLVVTERHF  
FAAGQNOLLIIVDSDVSADGKYTCESMNTLTERGNVRSLSVIPTPTCDSPQMTPAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWWVIIYHTRRRNEDCSITNTDETNLNPADIPTYLSSQGTIADRO  
LKGNVYGSDFPETYHTGCSPDPRTVLMDHYEPSYIKKCEYPCSHPSEESCRSFNSNISWPS  
HVRKLLNTSYNSHEGPGMNLCLNKSSLDFSANPEVASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLSGSEEDGKERTDFQEENHICTFKQTLENRYRTPNPFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

CAAAACTTGGCTCGCGGAGAGCGCCAGCTGTGACTTGAAAGGGAGCCCGAGCCCCGGAGCGCAGCTGAGAC  
TGGGGAGCGGTTCTGGCTGTGGGCGCGCTCGCGCGGGGCCAGCAGGGAGGGAAAGCTGTTGCTGC  
CTGCTCCACAGGGGCCACTGGTGTGAACGGGGAGGCCCTGGTGTCCCCTATCCCTTCTTATA  
GAAACCTTCACACTGGGAAAGGCAGCGGAGGGCAGGGGCTCATGTGAGCAAGGGAGGCCGCTGATCTGCAG  
GCCACAGCATTCCGAGTTTACAGATTTCACAGATAACAAATGGAAAGGGAGGCCGAAACAGCCTGCCGGT  
TCCATCAGGCCCTGGCGCCAGGGCAGCTGTGACTTCGGCACCCCGCTGCCAGGGCACCAGTGGCCAGAGGCCGGTGTCTGC  
TGGCTCTGCTGCTGCGGCCAACAGCTGCACTGGGACCTGTGCTGCGTGTGAGGGGCCAGGATTGGCCGA  
GTGCGGCCAACAGCTGAGGCCAGAGAAGCAATTGGGAGGGAGGCCGTGCTGTTACTGAGCCCTGAGG  
AGCCCGGGCTGGCCAGCGCGGTCTAGCTGGCCAGACCTGCTGAGCACCAACACCATACTCTGCAGAACACCAGC  
GCCGTATTGACCTGCGTAGTTGGGGGACCTGCTGAGCACCAACACCATACTCTGCAGAACACCAGC  
TGGAAAAGATCTACCTCTGGAGGAGCTTCCCGGCTGGAGACACTGAACCTGCAAAACACCCTGTA  
CTTCCGAGGGCTCCAGAGAGGCTTGGGACATGACCAAACCTCAATTACTGTAATTGGCCATAAACAGC  
TGACCTTGGCACCCCGCTCTGGCAAACGCCCTGATCAGTGTTGCAACTATCTCACCAAGATCT  
ATGGGTCTACCTTGGCCAAGACCAAACTTGGGCTGTGACTCTGGCACAAACAACAGCTGGCAGACGCCGGC  
TGGCGACACACATGGTCAACAGGCTCCGCAAGCTGCGAGGCTCTCATCTGTCAGAACACTTCTGCGCAGCTG  
CCAGCAGCTGCCCTGCAAGCTGAGGACTAACAGGCTGGAGAACAGTGGAGAAAGATCCCCCGGGGCT  
TCAAGCAGGCTGAGCAGCTGGGAGGACTATGGTCAAGGAGAACAGGCTGGAGAACAGTGGAGAAAG  
CTTCTGGAGAAGCTCCAGGAGTCTGGAGTACCTGGAGTACCTGGAGAACAGGCTGGAGTCCAGGCTGG  
CGGGCACCTGGTGTCTGCACTTGGAGAAGAACCCGATTCGGAGCCTGGAGGAAATGTGCTGACCCCATCC  
GCAGCCTGGAGTACCTGCTGCAAGCAACAGCTCGGGAGCAGGGCATCCACACTGGCTTCCAGGGCC  
TCAAGCAGGCTGAGCACACGGCTGACAGGACAAACGCCCTGGAGGGAGCTGGCGTGCCTGCCGGTGC  
GCACCCACCTGATGCTGCAACAGGATCAGGCTTGGCCGGAGAACACTTGGCACACACTTCTCTGGAGG  
AGCTCAACCTCAGGCTAACACGGCTCACCCAGGCCCCAGTGGAGCACCCTGGCGTGAAGCTGGCCCTGCTGC  
GCTCGTGGGACTCTGGGCAACGGGCTGCAACAGCTGGCACCTGGCGTGCCTGGCGTGAATGCTGCTG  
TCAAGGCGATAGACTGAGCTGGCTCTGGAGGGGGCTGGGGCATGGCTGAGCTGGGTGAGCTGTACCTCA  
CCAGCACCCGACTGGCACGGAGGCTGGGCCCTGGCTGGGTGACCTGGCGTGCCTGGCGTGAAGCTGGACA  
TCGGCGGGAATGACTGCTCACAGGATTCGGGCCCCAGGGCTGCTGGGTGACCTGGAGTACCTGTA  
AGATTAGTGGGCTGGCCCAATGCTTCAGCTCCAGCAGGCCCCAGGGATCTTCTCAGGTTAACAGC  
TGGCTGGGCTGGGCTGGGAGACTGGCTTCTGGGGAGGCTGAAGGACCTGGAGTCTGGAGATTGAAGG  
ACTAGAGTTGGTGAATTCAGGAGGAGCTGGCGCTTGGGAGGAAAGGGAGGAGGAGGAGGAGGAGGAGG  
AGGAAGAGGAAACAGAGTAGTGAACAGGTGATGAGCTGACCTGGAGTGTGGACCCGGGACTCTTCTGC  
AGACAGGCTGTGTGAGGCCCCACTCTGGCTGGTCAACAGAACACACCAGCTGCACACATGGCGA  
TCCACACATGACACGGCTGACAGCTCATACTCCCACCCCTTCCACAGGGCTGTCACAGGCCAGACACATGC  
ACACACATCACACCCCTAAACACCCAGCTGAGGACACAACTACCTCCAAACACACCAGCTGTCACAC  
CCCCACTAACGGCTGGCACGGCCCTCTGGATCATGAGGGAGGCTGGCCCTGGCGACACAGGCCACCA  
TTCCTCTCCCTGCTGCAATGTTGCTGATCATGAGGGATCCACAGGCTGGCGACACAGGCCACCA  
CAGGCCCTCAAAGCTATGGCACAGAGCTCTGGCCAGGAGAACATGAGGCTGGCGCTGCGCT  
GTCCATCTGTCCTGGCTCCCTGGAGAAGACAAAGGGTATCCAGTGGCTGTGGCGAGGTGCTGCCACCCCT  
GGACATCACAAAGCTGGCTTTATCTCTTCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
TGGCCACCCCTGCTCTCCAGGTGCTGGGAGCTGACTCTGCTAAGAGTCCCTCCCTGCCAGGCCCTGGAGGACA  
CAGGCACTTCTTCAATGGCAAGGCCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GTTCTTCAGGCCCTGGGGAGGTTCCGGTGCCTTATTCTTCTAAGGAAAAAAATGATAAAAT  
CTCAAGGCTGATTTTCTGTTAGAAAACATAATATAAGGATTATCCCTATCCCTGGCAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENFAEEEPVLVLSPEEPGP GPAVSCP RDACS QEGVVD CGGIDLREF PGDLP  
EHTNHL SLQNNQLEK IYPEELSRLHRLETI LNQNNR L TS RGLPEKA FEHLT NLYL ANN K  
LT LAPRFLP NALIS VD FA ANYL T KI YGLT FQ KPNL RS VY LHNN KLA DA GLP DNM FNG SSV  
EV LIL SSN FLR HVP KHL PP ALY KHL KNN KLE KIP PGAF SEL SS LRE LY LQNN YLT DE GLD N  
ET FWKL SS LEY LD LSS NN L SR VPAGL PRS L VLL HLE KNAIR SVD AN VLT PIR SLEY LLL HS N  
QL REQGIHPLA FQ GLK RL HTV HLYNN AER VP SGL PRR VRT L M ILHN QIT GIG RED FATTY F  
LEEL NLS YN RIT SPQ VHR DAF RK LRL RSL DLS GN RL H LT LPP GLP RNV HVL KV KR NEL A A LA  
RGAL AGMA QL RE LY L TS N RL RS R AL G PRA WVD LAH LQ L D IAGN QL TE I PEG L PES LEY L Y L  
QN NK I SA VPAN AFD ST PNL KG I F LRF NKL AVGS VV DSA F RRL KHL QV L DIE GN L EFG DIS K D  
RGR LGK EKE EEE EEE EEE ETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

# FIGURE 109

GGGAGGGGGCTCCGGGCGCGCAGCAGACCTGCTCCGGGCGCGCCTCGCCGCTGTCTCGGGAGCGGCAG  
CAGTAGCCCGGGCGGCCAGGGCTGGGGTTCTCGAAGACTCTCAGAGGGCGCTCCCCTCGGCCAACACCC  
CAACAGCTATCTCGCTCACCTCGAGGGCCACTGGCTGCCAGGCCAGTCCCAACATGGATTTCCTCTGGCTGGT  
GCTGGTATCTCGCTCACCTCGAGGGCCAGGCCAGTCCCAACATGGATTTCCTCTGGCTGGCTGGCAGTCTGGG  
TGCCCTATGCTGTATGGTGGGAGGATTGACTGCTGTGGGCTGCCCCAGTCTGGGAGCAGTGTGAGCC  
TGTGCTGTATGGTGGGAGGATTGACTGCTGTGGGCTGCCCCAGTCTGGGAGCAGTGTGAGCC  
AAAAACCTGTAACTCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTAAAGCACAGGTGCAAACTTA  
CGGCAGCTAACAGTGTCTACTGTCTAACCGGATAATAGCTCATGCCGATGGTTCTGCTCAAGTGCCTGACCTG  
CTCCATGGCCTAACCTGTCAAGTATGGCTGTTAGATGTGATGATGTCTCACAGGAAGAGCTCTGGCTTAGATT  
GCACCTGGCTCTGATGGGAGGACTGTGTAGATGTGATGATGTCTCACAGGAAGAGCTCTGGCTTAGATT  
TAGGCAATGTGTGCACTGGGAGGACTCATCTGGCAAGTGTCAAAAGGGCTTGATCTCATGTATATTGGAGG  
CAAATATACATGTCATGACATAGACAACTGTCACTGGTCAAGTGTCAAGCAGCTTGTCTGATGTTATAA  
CGTAGCTGGTCTTACAAGTGTAAAGGAGATAACAGGGTGTGACTGACTTGTGTGATATCCAAA  
AGTTATGATTGAACTCTCAGGTCCATTCTGATGATGAAAGTACTTGTGGCTTCAAGGAAACCCATTTAAAGGGTGACACAGAAA  
TATAAATTGGATTCTCTGATGTTGAAAGTACTTGTGGCTTCAAGGAAACCCATTTAAAGGGTGACACAGAAA  
CTGCCCTACACTGTCAGGCAACACCTTCAACCCCTAACCAACGGCAACACCAATTCTACTCCACCAACCAACCAAC  
CTGCCCTACAGGCTCAGAACACCTTCAACCCCTAACCAACGGCAACACCAATTCTACTCCACCAACCAACCAAC  
ACCACTGGCAGTCAACCTCAGGGAGGAGGATACTGGTCAAGTGTCAACAGGGTACAGACAGCCTCAGAAAACCCAGG  
AGATGTGTTCTGGTCAAGTGTAAATTGACCATGCTGATGGATGAGCAGGGAGAAAGACAA  
TGACTTCAGTGGAAACCAATCAGGGACCCAGCAGGTGGACAAATCTGACAGTGTGGCAGCAGGAAACCCAGG  
GGGAAAAGCTCAGCGCTTGGTGTACCTCTGGCCCTCATGCACTCAGGGACCTGTGGCTGTATTCTAGGCA  
CAAGGTGAGGGGGCTGCACTTGGCAACTCTGGCAACTCTGGGTTGTGAGAAAACACGGTGCACGGAGCAGCCTGTG  
GGGAGAAGATGTGAGGGTGTGGAGGAAACACAGATCACCTTGGGAGGCTGACATCAAGAGGGCAATCACA  
AAAGATGATTAAAGGGTTGGAAAAAAAGATCTATGTTGAAATTAAAGGAAACTTGGGATTATTGAGCTGGAGAAG  
AGAGACTGTAGGGGAAACCATGTGTTCTCAAGTATATGAGGGTTGGCACAGAGGGTGGCAGCAGCTG  
TTCTCATATGCACTAAAGATAGAAAGAGGAAACTGGCTTAGAGCTAGAGTATAAGGGAGCATTTCTGGCAGG  
GGCCATTGTTGAAACTCTCAAAAGGAAAGTGTGAAAATCTCATGTTCTCTCTCTTTCTAAAAAAATTAGA  
TAAAAATTTGTCATTTAAAGATGGTTAAAGATGTTCTTACCAAGGAAAGTAAACAAATTATAGAATTTCAAA  
AGATGTTTGATCTCTAGTAGTATGCACTGAGTAAATCTTGAAGAACTTAAATATGAGCTTAAAGGCTTAAATTAGG  
CATTTCCCTCTTGACCTCTAATGGAGGGATTGAAAGGGAGAGGCCACCAATGCTGAGCTCACTGAATA  
TCTCTCCCTATGGCACTTCAAGGCTTCAAGGAGGGATTGAAAGGGAGAGGCCACCAATGCTGAGCTCACTGAATA  
AGATATTCTTGTAGTATCTAGTAAATGCTCTAGTGTGGGGTTCTCAAGTGTCTCATGTTAAAGGTATAAGCC  
TTCTCATATGCACTGGATGATGTTCTAGGATTTTTTTAAAGAGATCTTCAAGGAAACAGTTCAGAGAG  
ATTCTCATGGGTGTCATTCTCTCTGCTGTGCAAGGTATCTTGTGCTGTGAGAAAGAGTGTGCTGGCTTCCCC  
ACACCGGCAGACCTTCTCTCACCTCATGCTGAGTATGTTCTCTTATCAATTGAGCTCTCCAGGTCCAC  
AGAACAGTAAATTCTTGTGAACTAGGTCAATGAGGCTTGTGAGTAAAGGGCAAAATATGGCTGTAGATCTTAACTGGTAAAGGGAGGGCTGG  
AGGGGGAAAATAATCAATTAGGCTTGTGAGTAAAGGGCAAAATATGGCTGTAGATCTTAACTGGTAAAGGGAGGGCTGG  
TCTCTTATGGTCATAACTGCACAGCTGAGGATGAAAGGGAAAATAATGAGTAAAGGGAAAATTAATGAGTAAAGGGAGGGCTGG  
TGATACATTGCACTAACTGTGGAGAGGTTATCCAAGTACTGTATTAACATCTGGTTTATTATTTAAAGTGTG  
CTTAAATAAAAAAATGTTAGTGGTTTCCAATGGCTAATAAAAACAAATTATGGTAAATAAAAACACTGTTGAGTAA

# **FIGURE 110**

MDFLLALVLVSSLYLQAAAEEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCPD  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYCDCVKGQIRCQCPSPGLHLAPDGRITCVDVDECATGRASCPFRQC  
VNIFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYCSSFARCYNRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNNWIPDVGSTWPPKTPYIIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPA AASTPPGGITVDN  
RVQTDPQKPRGDVFSLVHSCNFHDHGLCGWIREKDNDLHWEPIRD PAGGQYLTVAAKAPGG  
KAARLVLPLGLRMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQQTQI  
TLRGADIKSEQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTTGAAAGGATTATCACCTGATCAGGTTCTCTGCATTGGCCCTTAGATTGTGA  
**AAT**GTGCCCCTAAGGGCTTCAACATTCTTCTTCTTGTGCAACAGGTGCTTCGGGCTGA  
AGGTGAAGTGGCCCATCACACACTGTCTCATGGCGTCAGAGGTGCTGGCCCTACCTAACCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCAGACATCATGGCTATTGGAGAGACCCA  
ACAATGGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAATACC  
AACACAAGTTCACCATGTGCCACCAAACTGCATCTGTCTTATCACACCCACTGCAAGTTCCT  
GATGAGGCAATTACATCGTGAAGGTCACATTCTCAGGGAAATGGAACTCTATCTGGCAGTC  
GAAGATACAAGTCAGGGTGTGATGATCCTGTCAAAAGCCAGTGGTCAGATTCTACCTCCCT  
CTGGGCTGTGGAGTATGGGGAAACATGACCCATGACATGCGATGGAGGGGGACTCGG  
CTAGCTTACACATGGCTTAAAGGGAGACCTGTCCACACAGCTTCAACTACTCTTTC  
TCCCCAAAACAATACCTCTCATATTGCTCAGTAACCAAGGAAGACATTTGGGAATTACAGCT  
GCCTGGTGAAGGAACCTGTCACTGTGAATGGAAAGTGATATCATTATGCCCATCATATTAT  
GGACCATTTAGGCTTCAAGTGAATTCTGATATAAGGGCTAAAGAGTGGGGAAAGTGTACTGT  
TGACCTTGGAGAGGCCATTCTATTGTGTTCTGTGCTGATTCTCATCCCCAACACTCT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAAAGGT  
GCATCTGAGAAGATAGGCCAGAACAGACATGGACTATGTGCTGTGCTTAAACACATAAC  
CGGCAGGCAAGATGAAACTCATTTTCACTATTATCATCTTCCGTAGGACTGGAGAACGCTG  
CACAGAAAGGAAATCATGTGACCTTACAGGTTAACTGGAATATCACTATTGTTGATT  
ATATCCATGTGCTTCTCTCTATGGAAAAAAATATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGGCAGAACAGAAATCAGGAAAGCTAACACATTCTCAGGGCATAGATG  
CTCTGGATGACTTCCGAATATGTAATTGTTGCTTCTCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCCTGTTCCAGCCTGATTGTGTATGGGCAAGATTGACAGTACAGT  
GTATGAAGTATTACAGCAACATCCCTGCCAGCAGAACCCATCCAGAGT**GA**ACTTCTCATGG  
GCTAAACAGTACATTCTCAGTGAAGAAACCCAGGACCAACACCTCTTACTCATTTCTTAC  
ATATTAATCTGGAATCAGTGAAGAAACCCAGGACCAACACCTCTTACTCATTTCTTAC  
TGCAAGATAGGGCATTATGCAAAATTGACTGCGAGTTTTCTCAGCATATACACATGTCTT  
GTGCAAGAGAAAACATGTTGGGAAATATTCTCAGTGGAGACTGGCTCTCATGTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAAAGTTGTGATGAAATATTCTCATACACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCTGTCTCACCTACAAA  
TGTGGAAACATTCTACATTGTGCTGATTCTCAGCAGACTTGTGTTTATTAAAGTTTATTAGT  
TTAAGAATGCTCAATTATTATGTTCAATTTTATTCCAAATTCTCATCTGTGTTATTGTCACAA  
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTCTCTTTTTCAATCACC  
AGTAGTATTGAGAAGAACGACTTGTGACAGGTTCTAAGGAAGTACTTAAAGTCTTATT  
TTTTTCTCAAGGAAAGATGTTCAATTATTCTGTTTTCTGTTTTCAATT  
~~~~~

## FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPNASCILLINPLQFPDEGNYIVKVNIQGNGLSASQ  
KIQVTVDPPVKPVVQIHPGSAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTSFS  
PQNNTLHIAPVTKEIDIGNYSCLVRNPVSEMESEDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAIALFDCSADSHPPNTYSWIRRTDNNTYIIKHGPRLEVASEKVAQKTMVDYVCCAYNNIT  
GRQDETHEFTVIIITSVGLEKLAQKGKSLSPLASITGISLFLIIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPRSVPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 113

GCAAGCGGCCGAATGGCGCCCTCCGGGAGTCTTGCAGTCTCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGTCCCCTGGACGGCGGGAGAACGTTCGCTCATCACGGACGAGA  
ACTGGAGAGAACCTGCTGGAAGGAGACTGGATGATAAGAATTATGCCCCGTGTGCCCTGCT  
TGTCAAAATCTAACCGGAATGGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGGAAAAGTAGATGTCACAGAGCAGGAGCTGAGTGGACGGTTATCATAACTGCTC  
TTCCCTACTATTATCATTTGTAAGATGTTGAAATTAGGGCCTATCAGGGTCCAAGGACTAAAG  
AAGGACTTCATAAACCTTATAAGTGTATAAGAGTGGAGAGTATTGAGGCCGTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGGA  
TCAGGACGTGCCATAACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTGGCTTAGCAACTCTGTTCCGACTGTATTAGGACTCTGTATGATAATTGTGC  
AGATTGCCATTGCTTCAAAAAGGCCAGACACAGCCATACCCATACCCCTAAAAAAAT  
TATTATCAGAACATGTCACACCCATTGAAAAGTGGAGGAGAACAGAGGCCGGTAGAGAA  
GATGTTTCAGAAAAGAAGCTGAAAGTAAAGAAGGAAACAACAAAGACTTTCCACAGATGC  
CATAAAGACAACGCTCTGGGCCATCATGGCCACAGATAAAATCTCTAGTTAAATTATAG  
TTATCTTAATATTGATTGATAAAAACAGAAGATTGATCATTTGTTGGTGTGAAAGT  
AACCTGACTTTTTGAAATTCAGGGTTCACTGCTAGATTGTCATTAATTGAAAGACTTA  
CATTAGAAACATAAAAGCACTAGGTATACTAAGTTGAAATATGTTAAGCACAGTATGATG  
GTTAAATAGTTCTCTAATTTTGGAAAATCTGCCAAGCAATAAGATTATGTTATATTG  
TTAATAAAACCATTTCAAGCTGAGTTGAAAATTCACATTTCCAAGTATTGATTAT  
TGAGGTATTAAAGAAGATTATTAGGAAAATATTCTCATTTGATAATAATTCTCTG  
TTCACTGTTGAAAAAAAGAAGATAATTCCCATATAATGGGAGTTGCCATTGTCAG  
AAATGTTGATTCACTGACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCTCTG  
ATTTTAGGTATTGCAACTAAACCTGGTCTTACATTAATTACAGTTTCTACACA  
TGTTAATACAGGATATGCTACTGATTAGGAAGTTTAAAGTTGATGTTCTGATT  
CAAACAAAGTTGATTCTCTGTATTCTTACTTACTATGGTTACATTTTTATT  
CAAATTGGATGATTTCTGGAAAACATTTTATGTTAGTAAACAGTATTGTTGTT  
GTTTCAACTGAAGTTACTGAGAGATCATCAAATTGACAATCTGTTGATAATTAAAATT  
TTGGCCACTTTTCAGATTTCATCATCTTGTGAACCTCACTGAAATTGTTTTT  
TTCTTTGGATGTTGAAAGGTAAACATTCTGATTTCTGATGTTGAAAAAGCCTGGTA  
TTTACATTGGAAAATCAAGAAGCTTAATATAAAAGTTGATTCTACTCAGGAAAAG  
CATCTCTGTATATGCTTAATGTTGATTCTCTCATATAACAGAAAGTCTTAATTGAT  
TTACAGTCTGTAATGCTTGATGTTAAAATAAACATTTTATATTTTAAAAGACAA  
ACTTCATATTATCTGTTGATGTTCTGACTGGTAATATTGTTGCGGATTTCACAGGAAAA  
GTCAGTAGGATGGAACATTTACTGTTTAAAGAGCTAGAAATACATAGTTT  
CACCTTAAAGAAGGGGAAAATCATAAATACAATGAATCAACTGACCATTAACGTTAGAC  
AATTCTGTAATGTCCTTCTGAGGCTCTGTTGCTGTGAATCATTAGATTACAG  
TATCTGTAATATACAAGTTCTTAAAGCCCTCCTTATGAAATTAAAATATTGTCACATT  
AAAGAGTTGGATGTTGTAACTTGTGATGCCCTAGAAAATATCTAACGACAAAATAAACCT  
TTCTAACCACTTCATTAAGCTGAAAAAAAAAAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIKVADCLCP SKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTN KDPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## FIGURE 115

GGCAGTGTCCAGCTGCGGAGACCCGTGATAATTCTTAACAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAACCGCAAGCAGTTGCTAACCCAGTGGACAGGGGATTGGAAGAGCGGG  
AAGGTCTGCCAGAGCAGTGTGACACTTCCCTCTGTGACC~~AT~~GAAACTCTGGGTGCTGC  
ATTGTGATGGCTGGTTGGTCTGAGCTGTGCAAGGCGAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTTATGAGAGAAGAGCTGGTCAGTCTGAAAGAGTACATC  
CTTGTGAGGAAGCCAAGCTTCAAGATTAGAGCTGGCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGTACCTGGCTACCCCTGTGAATGCCAACAACTGG  
TGAAGCGGCTAAACACAGACTGCGCTGGAGGACCTTGTGCAAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGCAAGCGCAGTTCTCCACTGATGAGGACGAGATAGG  
AGCTGCCAACGCCCCATGAGAACACTTCAGGACACATCACAGGCTGACCCAGGCCAACATTCA  
GAGGGAACTTCCAGGAACCAAGTACCAAGGAACTGAGGTGGATGACTGCTTTGGATG  
GGCCGCTGGCTACAATGAGAGGACTATTATCATCGCTGAGGATGGAGCAGGTGCT  
AAAGCAGCTTGTGCGGGGGAGGAGGACACCAACAAACAAAGTACAGGCTGACTACCTCA  
GCTATGCTGCTCCAGTTGGTGTGACCTGACCCGTGAGCTCACCGCCGCGCTGCTC  
TCCCTTGACCCAACCGAACAGCTGGAGGAAATCTGCGGTACTTTGAGCAGTTATGGA  
GGAAGAGAGAGAACCTGAAACATCAGACAGAACCTGACTAACACCCAGAACGCA  
TCTATGAGAGGCTGTGGACTACCTGCTGAGAGGGATTTACGAGAGCCCTGCTGCTGG  
GAGGGTGTCAAACACTGACACCCCGTAGACAGAAAGAGGCTTCTGTAGGTACCAACCCATGGCA  
CAGGGCCACACGCTGCTCATGGGCCCCCTCAAAGAGGAGGACGAGTGGACAGGCCACCA  
TCGGTCAAGGACTACATGATGTCATGATGAGGAATCGAGAGGATCAAGAGGATCGCAAAA  
CCTAAACTTGACGAGCCACCGTGTGATCCAAGACAGGAGTCTCACTGTCGCCAGCTA  
CCGGTTTCCAAAAGCTCTGCTAGAGGAAGATGACCCCTTTGTGGCCCGAGTAATC  
GTCGGATGAGCATATCACAGGGTAAACAGTAAAGACTGCAAGATTGTTACAGGTTGCAAT  
TATGGAGTGGGGAGGACAGTATGAACCGCCTTCAGACTTCTCTAGGGCACCTTTGACAGCGG  
CCTAAACAGAGGGGAATAGTTAGCGACCTTCTAAACTACATGAGTGTAGAAGCTG  
GTGGTGGCCACCGCTTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGTACAACCTTGTGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCC  
TGTGTTGTGGCTGCAAGTGGCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAACAGGTTGACTGAC~~AT~~CATCCTTTCTGTCTTCCCCTTCTGGTC  
CTTCAGCCCCATGTCAACGTCAGACAGACACCTTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCAGTCTGT  
GTGACTGAAAGTCCCAGCCCTTCATTCAAGCTGTGCCATCCCTGGCCCAAGGCTAGGATCA  
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCTAGTCAACAAAGTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGTTACCAAAAAATAATGTCCTACAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVVEAKLSKIKSWA  
NKMEALTSKSADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTRYLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRAELTRRLLSLDPSHERAGGNLR  
YFEQQLLEEEERKTLTNQTEAEALATPEGIYERPVVDYLPERDVYESLCRGEVGVLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLA RATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYVGGQYEPHFDFS  
RRPFDSGLKTEGVRNLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

### **FIGURE 117**

## FIGURE 118

MRLSSLLALLRPALPLILGLSCLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSSRARLD  
QSDEDFKPRIVPYRDPNPKYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHPFRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETRLHLHHTFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPPLL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERYPG  
TRLAFLAVRAEAPSQRVLMDVSVSKHPDTLFFFITVWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFPALSPQRSPPGPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGOEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAGQLAMALMFEEQEQANST

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 489-507

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGCAGCTGCCTTCCTGTCCCCAAGCC  
GTTCTAGACGGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTG  
AAGCATTTCTGCTTGTACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTAACAGCTAACAAAAGAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCAGTATACTGTATTATCCTGTAAACC  
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGACCAACACTGTGACAAGCAG  
AGTTCTCAGTTCTGAAATGTTAAAGTGTGAGTCAATTAAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATAACATG  
GTTCTTCCCTTGACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTTGTTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAATCAATGAAAAGACTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCTGAAATATGCTGGAGTATTGCAAGAAAATGCAAGAGATGCTGATGGA  
AAAGATGTATTAAACACAAATCTGTTGGGTTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTTGGCATTTCATTTCAAT  
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATATCCAA  
TACAGCTGTATGTTCTTTCTAAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTTAAACACATGAACATTGTAATG  
TGGTGGAAAAGAAGTGTAAAGAATAATAATTGCAAAATAACTATTAAATAATTATAT  
GTGATAAAATTCTAAATTGAACATTAGAAATCTGTTGGGCACATATTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTGTGTTGCTGTTCCCTTACTCTAAACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCTTCAAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSENKVVFESINMDTNDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRILNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMVMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

CCACGCGTCCGATCTTACCAACAAACACTCCTGAGGGAGAAAAGAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAAATGATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTCTCTTCCCAAATGTTCTATGGACTGTTGCT  
GGGATCCCCATCTATTCTCAGTGCCTGTTCATCACCAGATGTGTTGACATTCGCAT  
CTTCAAACCTGTGATGAGAAAAAGTTCACTGAGAATTTCACAGAGCTCTCTGCT  
ACAATTATGGATCAGGTTCACTGAGAATTGTTGTCATTGAACGGAAATATTTCAATCC  
AGCTGCTACTCTTTCTACTGACACCATTCCTGGCGTTAACGTTAAAGAACTGCTCAGC  
CATGGGGCTCACCTGGGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTCTACAAGA  
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTGACAAAGTCTTGAGCTCTGGGATGTAAGGGAGCCAAACAA  
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAAGGCAAAATTGGA  
ATGATGTAACCTGTTCTCAATTATTTGGATTGTGAAATGGTAGGAATAATCCTTG  
AACAAAGGAAATCTTTTAAGAACAGAACGGCACAACCTCAAATGTGAAAGAAGGAAGGAGCA  
AGAACATGGCACACCCACCGCCCCACAGAGAAATTGTCGCGCTGAACCTCAAAGGACTTC  
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAA

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS  
NPRQNWNNDVTCFNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

## FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPPLRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPFRFNSSFHLNSETGTLVFTAVHKDDSGQQYCIASNDAGSARCEEQEMEVYDLDNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267